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Perfect score:
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/cgn2_6/ptodata/2/pubpaa/rcTUS_PUBCOMB.pep:*
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10 US-09-864-761-38710

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10 US-09-864-761-4737

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10 US-09-864-761-4597
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US-09-815-626-6

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US-09-822-687-6

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US-09-915-626-12

US-09-925-300-977

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Sequence 123, App. Sequence 42876, A Sequence 46, Appl. Sequence 38710, A Sequence 47370, A Sequence 47370, A Sequence 322, App. Sequence 3283, A Sequence 41907, A Sequence 41907, A Sequence 41907, A Sequence 41907, A Sequence 43513, A
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Sequence 12, Appl
Sequence 97, App
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Sequence 35556, A	~		Sequence 45498, A		Sequence 10, Appl	49065,	Sequence 1412, Ap	Sequence 48030, A		415	Sequence 819, App	819,	181,	Sequence 181, App	Sequence 181, App	Sequence 47726, A	Sequence 1841, Ap	Sequence 38701, A	-	Sequence 47802, A	Sequence 48392, A	Sequence 1688, Ap	Sequence 39317, A	Sequence 618, App	Sequence 47172, A

ALIGNMENTS

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Query Match
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Sequence 30, Application US/09789404
Patent NO. US20020025554A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
CTITLE OF INVENTION: NOVEL LEUCINE RICH REPEAT-CONTAINING MOLECULES AND USES
FILE REFERENCE: 10448/008001
                                                                                                                                                                                                                                                       US-09-815-626-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-09-789-404-30
Sequence 6, Application US/09815626
Patent NO. US20020076752A1
GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria Alexandra
TITLE OF INVENTION: 3395, A NOVEL HUMAN LEUCINE-RICH REPEAT
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-031001
CURRENT APPLICATION NUMBER: US/99/815,626
CURRENT APPLICATION NUMBER: US/09/815,626
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,863
PRIOR FILING DATE: 2000-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/456,592
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 30
LENGTH: 49
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/789,404
CURRENT FILING DATE: 2001-02-20
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Pred. No. 0.00017
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es 17;
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                                                                                                                                                                                                                                                                                                                                                                                                        US-09-789-404-6
US-09-789-404-6
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 6
LENGTH: 54
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APPLICANT: Khodadoust, Mehran
                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09789404 Patent No. US20020025554A1
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SEQ ID NO 6
LENCTH: 54
TYPE: PRT
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Best Local Similarity
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                                                                                                                                                            TITLE OF INVENTION: NOVEL LEUCINE RICH REPEAT-CONTAINING MOLECULES AND USES THEREFOR FILE REFERENCE: 10448/008001
CURRENT APPLICATION NUMBER: US/09/789,404
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/456,592
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEO ID NOS: 30
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TITLE OF INVENTION: 31939, A NOVEL HUMAN LEUCINE-RI
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-038001
CURRENT APPLICATION NUMBER: US/09/822,687
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quence 6, Application US/09822687 atent No. US20020076753A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/193,919
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 10
                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                   OTHER INFORMATION: consensus sequence
                                                    ORGANISM: Artificial Sequence
                                                                                   TYPE: PRT
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                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NPFNCDCELRWLLRWLRETNPRRLEDQEDLRCASPESLRGQPLLELLPSDF
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Pred. No. 0.0018;
7; Mismatches 22;
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Pred. No. 0.0018;
7; Mismatches 22; Indels
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; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-977
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US-09-925-300-977
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US-09-815-626-12
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Best Local S
Matches 16
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Matches 18; Conserv
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Matches 10; Conserv
                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. SEQ ID NO 977
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CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,863
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEO ID NOS: 17
                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US00/05988 PRIOR FILING DATE: 2000-03-08 PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/925,300 CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Glucksmann, Maria Alexandra
TITLE OF INVENTION: 33395, A NOVEL HUMAN LEUCINE-RICH REPEAT
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-031001
                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acids, Proteins FILE REFERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Craig Rosen, APPLICANT: Steve Ruben
                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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nes 16; Conserv
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                                                                                      Score 57;
Pred. No.
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Pred. No. 0.027;
9; Mismatches 22;
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                                                                          Mismatches
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RESULT 9
US-09-764-877-1144
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; LOCATION: (62)
; OTHER INFORMATION: Xaa equals stop translation
US-09-739-907-98
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US-09-764-877-1630
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: 60/070,567
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/070,692
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/070,704
PRIOR APPLICATION NUMBER: 60/070,704
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1630
LENCTH. 7
Sequence 1144, Application US/09764877 Patent No. US20020147140A1
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Best Local :
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Patent No. US20010012889A1
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                                                                                                                                                                                                                                                                                                                                                    LENGTH: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/739,907 CURRENT FILING DATE: 2000-12-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: 36 Human Secreted Proteins
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at Local Similarity
atches 10; Conserv
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TYPE: PRT
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                                                                                                        4 ARPPWMWVLCALITALLLGVTEHVLANNDVSCDHPSNTVPSGSNQDLGA 52
                                                                                                                                                                                             Local Similarity
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                                                                                                                                           9 ARPLWAWFQRARV-----
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Pred. No. 25;
                                                                                                                                                                                             Score 49; DB Pred. No. 30;
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; ORGANISM: Homo sapier US-10-001-883-123
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Best Local Similarity 3/...
Thes 15; Conservative
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NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1144
LENGTH: 91
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nuc
FILE REFERENCE: PC005
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Pluta, Jason
                                                                SOFTWARE: Pai
SEQ ID NO 123
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CURRENT FILING DATE: 2001-01-17
                                                                                             PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 137
                                                                                                                CURRENT APPLICATION NUMBER: US/10/001,883
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,059
PRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                 APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating
FILE REFERENCE: DEX-0271
                                                                                                                                                                                                                                    APPLICANT:
                               LENGTH: 42
TYPE: PRT
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LOCATION: (57)
OTHER INFORMATION: xaa equals any
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LOCATION: (25)
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                                                                                  PatentIn version 3.1
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Pluta, Jason
Ghosh, Malavika
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SEQ ID NO 42876
LENGTH: 50
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Best Local Similarity
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                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 4911
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OTHER INFORMATION: MAP TO AF161326.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL =
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL =
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
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                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                               FILING DATE: 2000-06-30 APPLICATION NUMBER: US 09/774,203
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                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 60/236,359
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FILING DATE: 2001-01-30
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Chen, Wensheng
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                                                                                                                                                                                                                                  Sequence Listing Engine vers. 1.1
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Pred. No. 30;
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RESULT 13
US-09-864-761-38710
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Best Local S
Matches 12
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SEQ ID NO 46
LENGTH: 77
TYPE: PRT
ORGANISM: Triticum aestivum
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Best Local :
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                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/95: CURRENT FILING DATE: 2001-09-11 PRIOR APPLICATION NUMBER: 60/232,569 PRIOR FILING DATE: 2000-09-13 NUMBER OF SEQ ID NOS: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Antimicrobial Peptides and Methods TITLE OF INVENTION: Use
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Simmons, Carl R. APPLICANT: Navarro, Pedro
                                                                     PRIOR APPLICATION NUMBER: GB 24263.6 PRIOR FILING DATE: 2000-10-04 PRIOR APPLICATION NUMBER: US 60/236.3 PRIOR FILING DATE: 2000-09-27
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PRIOR APPLICATION NUMBER: US 60/207,456
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                                                                                                                                                              PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: US
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                                    PRIOR
                                                        PRIOR
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OTHER INFORMATION:
OTHER INFORMATION:
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                                APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
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12; Conser
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DATE:
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                   NUMBER:
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EST_HUMAN HIT: A1632488.1, EVALUE 3.00e-21
SWISSPROT HIT: P05998, EVALUE 3.10e-01
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                 PCT/US01/00667
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Pred. No.
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APPLICATION NUMBER: FILING DATE: 2001-0: FILING DATE: 2001-01-30 APPLICATION NUMBER:

2001-01-30

PCT/US01/00669 PCT/US01/00664

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PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
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Matches
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION,
FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
OTHER INFORMATION: SWISSPROT HIT: P50343, EVALUE 9.20e-01
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TYPE: PRT
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FILING DATE: 2001-01-29
R OF SEQ ID NOS: 49117
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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10; Conservative
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PRIOR FILING DATE: 2000-02-04
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-92,
PRIOR FILING DATE: 2000-92,
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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US-09-864-761-47370
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LENGTH: 61
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Best Local
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APPLICANT:
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CURRENT FILING DATE: 2001-05-23
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
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PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 47370

LENGTH: 52

TYPE: PRI

OTHER INFORMATION: EXPRESSED IN NAULT LIVER, SIGNAL = 0.59

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59

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Mouse TANGO 393 Le
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Protein sequence S
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AAB40541	AAU64105	AAM84924	AAU48483	AAE03946	AAU63604	AAU45258	AAU50568	AAU57157	AAU53141	AAY38427	AAU55639	AAU49947	AAB29193	AAG00181	AAU66070	AAU58161	AA007825	ABB03683	ABP09568	ABP08373	ABB08809	AAY11476	AAB38009	AAU61143	ABG21804	AAU39937	AAU49313	78	642	AAB56399	ω.	6538	642	. AAG65814
Human ORFX ORF305		Human immune/haema	nibacter	Human gene 49 enco	Propionibacterium	Propionibacterium	Propionibacterium	Propionibacterium		Human secreted pro	Propionibacterium	Propionibacterium	Protein encoded by	Human secreted pro	Propionibacterium	0		muscu	ORFX	ORFX pro	pro		Human secreted pro	Propionibacterium	Novel human diagno	Propionibacterium	Propionibacterium			state ca	Amorphous domain o	Propionibacterium	opionibacterium	33395 LRR domain C

ALIGNMENTS

RESULT 1 AAB87100 ID AAB8

AAB87100 standard; Protein; 51

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AAB87100;

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PTTXRX
Nucleic acids encoding secreted TANGO and MANGO polypeptides, useful for the prevention, diagnosis and treatment of, e.g. cancers and immune
                                                                                                                                                                                                                                          Secreted protein; transmembrane protein; TANGO; human; drug screening; activity modulator; expression modulator; cancer; immunological disorder; cytostatic; immunomodulatory; gene therapy.
                                       WPI; 2001-138647/14.
                                                               Fraser CC,
Pan Y;
                                                                                                 (MILL-) MILLENNIUM PHARM INC
                                                                                                                        30-JUL-1999;
                                                                                                                                                 31-JUL-2000; 2000WO-US20935.
                                                                                                                                                                         08-FEB-2001.
                                                                                                                                                                                                WO200109162-A2.
                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                             Human TANGO 393 Leu-rich-repeat domain, SEQ ID NO:88
                                                                                                                                                                                                                                                                                                                       04-MAY-2001 (first entry)
                                                                         Sharp JD,
                                                                                                                          99US-0365164
                                                                          Kirst SJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           murine TANGO 393 is also included within the scope of the invention. The invention also encompasses fragments and variants of the proteins of the
                                                                                                                                                                                                                                                   Fraser Pan Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secreted protein; transmembrane protein; TANGO 393; mouse; murine drug screening; activity modulator; expression modulator; cancer; immunological disorder; cytostatic; immunomodulatory; gene therap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 253;
                                                                disorders
                                                                                                                                                                                        WPI; 2001-138647/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200109162-A2
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                                                                                       Nucleic acids encoding secreted TANGO and MANGO polypeptides, useful for the prevention, diagnosis and treatment of, e.g. cancers and immune
                                                                                                                                                                                                                                                                                                                                                                                                           30-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus.
                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     بر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NPWACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDLRALREADFQAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPWVCDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGC
                                                                                                                                                                                                                                                                             cc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                393
                                                                                                                                                                                                                                                                                Sharp JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                           99US-0365164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leu-rich-repeat domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332pp; English.
                                                                                                                                                                                                                                                                                Kirst SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 177; DB 22;
Pred. No. 8.7e-16;
4; Mismatches 16;
                                                                                                                                                                                                                                                                                Barnes TM, Wrighton N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunomodulatory; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      murine;
                                                                                                                                                                                                                                                                                   Myers PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Disclosure;

Page 266;

332pp; English

treating cen-

Novel Nogo receptor homolog polypeptide, NgR2 or NgR3, useful for treating central nervous system disorder, cerebral injury, spinal

cerebral injury, spinal cord

and demyelinating diseases

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ARCSULF 3
ARO21485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel secreted/transmembrane proteins, and concleic acids encoding them. The novel proteins are designated TANGO 339, CC TANGO 353, TANGO 358, TANGO 355, TANGO 368, TANGO 383, TANGO 383, TANGO 393, TANGO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               multifocal leukoencephalopathy; panencephalitis; Spongy degeneration; Alexander's disease; Canavan's disease; metachromatic leukodystrophy; Krabbe's disease; immune; bait protein; genetic mapping; gene therapy; transgenic animal; unregulated cellular growth; cancer; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NgR2; NgR3; axonal growth; central nervous system; CNS; cerebral injury; spinal cord injury; stroke; demyelinating disease; multiple sclerosis; monophasic demyelination; encephalomyelitis, Marchia disease; monophasic demyelination; encephalomyelitis, Marchia de Goografion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus NgR LRRCT domain protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAO21485 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-OCT-2001; 2001WO-US31488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200229059-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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                                                                                                                                                                                                                                               Strittmatter SM, Cate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NPWVCDCRARPLWAWLQKFRGSSSEVPCNLPQRLADRDLKRLAASDLEGC
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                                                                                                                                                               2002-416677/44
                                                                                                                                                                                                                                                                                                                       ) UNIV YALE.
) BIOGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.0%;
                                                                                                                                                                                                                                               RL,
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                                                                                                                                                                                                                                               Sah DWY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 167;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
L.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a Nogo receptor homologue polypeptide, NgR2 or CC NgR3, comprising a 50 amino acid LRRCT sequence, a 284 amino acid NTLRRCT CC sequence, or a 420, 461 or 392 amino acid sequence, all given in the Sequence, or a 420, 461 or 392 amino acid sequence, all given in the CC specification. The NgR3 protein or its binding antibody is useful for CC decreasing inhibition of axonal growth of a central nervous system (CNS) concuron, by contacting the neuron NgR3 or its antibody, and for treating CC NS disease, disorder or injury. NgR3 or a vector comprising NgR3 is cuseful for treating cerebral injury, spinal cord injury, stroke, CC demyelination, encephalomelitis, multiple sclerosis, monophasic CC demyelination, encephalomelitis, multiple sclerosis, monophasic CC Relation, encephalomelitis, as a bait protein of inducting an immune response in a CC mammal against NgR3 is useful for inducting an immune response in a CC mammal against NgR3 is as abit protein in a two-hybrid or three-hybrid assay, and as a research tool for identification, characterisation and CC sequences of the invention, characterisation and sequences of the invention, characterisation and cCC vector containing NgR3 is useful for producting non-human transgenic CC NgR3, for localisation and/or quantitation of NgR3, and for diagnostic CC antibodies are useful for treating or preventing unregulated cellular CC consensus NgR LRRCT domain of the invention. This sequence represents the cconsensus NgR LRRCT domain of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                          prostate cancer; genitourinary system carcinoma; testicular tumour; Alzheimer's disease; dementia; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; pepilepsy; psychiatric disorder; mania; depression; schizophrenia; anxiety; phobic disorder; learning disorder; memory disorder; amnesia; migraine; protein-protein interaction; cellular activity; neoplastic transformation; drug screening; forensic identification; gene therapy.
                    (MILL-) MILLENNIUM PHARM INC
                                                                      08-DEC-1999;
                                                                                                                 07-DEC-2000;
                                                                                                                                                                                                                  W0200142286-A2
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNS disorder; central nervous system disorder; prostate disorder; prostatitis; benign prostatic hyperplasia; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; leucine-rich repeat; LRR; AZAD; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human AZAD protein C-terminal leucine-rich repeat sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE03627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE03627 standard; peptide; 49 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NPWACDCRARPLWAWFORARVSSSDVTCATPPEROGRDLRALREADFOAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NXWXCXCRARXLWXWXXXXRXSSSXVXCXXPXXXXGXDLXXLXXXDXXXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al Similarity 46.(
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 AA;
                                                                                                                    2000WO-US33140
                                                                    99US-0456592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 126; DB 2
Pred. No. 4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50
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AAB82379;

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Homo sapiens

JAFFA; human; fibroblast growth factor

Protein sequence SEQ ID NO.30 23-JUL-2001 (first entry)

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders e.g. amnesia or age-related memory loss, and neurological disorders e.g. migraine. AZAD molecules are useful as markers of disorders or disease states, as markers for precursors of disease state or precursors of disease state or as markers of drug activity or pharmacogenomic profile of a subject. The AZAD polypeptide and polynucleotide are capable of modulating protein-protein interaction, e.g. by interacting with an extracellular component, thereby modulating e.g. by interacting with an extracellular component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Khodadoust MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neoplastic transformation and tumour progression. AZAD proteins are useful as immunogens to raise anti-AZAD antibodies which are useful to detect and isolate AZAD proteins and modulate its activity. AZAD proteins are useful to screen for naturally occurring AZAD substrates and to screen for drugs or compounds which modulate AZAD activity. AZAD nucleic acid fragments are useful as primers or hybridisation probes for the detection of AZAD-encoding nucleic acids. CDAA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cellular activities, including attachment, adhesion, migration, patterning, growth and/or differentiation of a cell. AZAD proteins regulate embryonic development and differentiation, tissue maintena and function, pathological conditions, e.g. neuronal degeneration,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carcinomas and testicular tumour). The neurodegenerative disorders include Alzheimer's disease, dementias related to Alzheimer's disease, Parkinson's disease, multiple scierosis, amyotrophic lateral scierosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorder (e.g. neurodegenerative disorders, including CNS disorders) and a prostate disorder, e.g. prostatitis, benign prostatic hyperplasia and cancer (e.g. adenocarcinoma, prostate cancer, genitourinary system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New leucine-rich repeat-containing protein and nucleic acid molecules for diagnosing, treating neural disorders, such as neurodegenerative disorders, such as Alzheimer's disease, dementia, epilepsy and prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the AZAD protein are useful in gene therapy. AZAD sequences are also useful to map their respective genes on a chromosome, for tissue type and in forensic identification of a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epilepsy, psychiatric disorders e.g. depression, schizophrenic disorders, mania, anxiety or phobic disorders, learning or memory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the C-terminal leucine-rich human AZAD protein which is a multiple leucine-rich
                                                                                                                                                                                                                                                                  AAB82379 standard; Protein; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing AZAD-mediated or related disorders, which includes a neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZAD proteins and nucleic acid molecules are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted protein AZAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 4; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-381633/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secreted protein. AZAD polypeptide is useful for identifying a compound which modulates its activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local 21;
                                                                                                                                                                                                                                                                                                                                                                               \mathbf{L}
                                                                                                                                                                                                                                                                                                                                                                                                                    1 NPWACDCRARPLWAWFQ--RARVSSSDVTCATPPERQGRDLRALREADFQAC 50
                                                                                                                                                                                                                                                                                                                                                                          NPFHCDCQLLPLHRWLTGLNLRVGA---TCATPPNARGQRVKA-AAAVFEDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 91; DB 22;
Pred. No. 0.00015;
8; Mismatches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for treating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    maintenance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE13009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human JAFFA polynucleotides (see AAR90326) and polypeptides (see AAR82351). JAFFA is a novel member of the fibroblast growth factor family. JAFFA proteins may be useful for developing novel diagnostic and therapeutic agents for JAFFA-associated disorders such as cancers and ABO(H) blood group disorders, and for controlling cellular proliferative and/or disorders. JAFFA nucleic acids and proteins may be used to treat and/or diagnose a variety of immune disorders such as cancering a such as a cancering a such as a cancering a continuate disease and multiple sclerosis. JAFFA nucleic acids may controlled a cancering a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                     cell proliferation; differentiation disorder; cancer; neuronal disorder neurological disorder; demyelinating disease; multiple sclerosis; degenerative disease; luntington's disease; spinocerebellar degeneration; nervous system; bone disorder; spinocerebellar degeneration; nervous system; bone disorder; osteoporosis; immune disorder; rheumatoid arthritis; diabetes mellitus; cardiovascular disorder; liver disorder; viral disease; pain; metabolic disorder; chromosomal mapping; tissue typing; forensic biolog cytostatic; nootropic; neuroprotective; anticonvulsant; osteopathic;
                         11-OCT-2001
                                                                              WO200175105-A2
                                                                                                                                Homo sapiens.
                                                                                                                                                                                     antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                               Human; leucine-rich repeat; LRR; 31939 protein; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus C-terminal leucine-rich repeat (LRRCT) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE13009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 136; 137pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated JAFFA nucleic acid molecules which encode novel fibroblast growth factor family members (JAFFA) are useful for developing novel diagnostic and therapeutic agents for JAFFA-associated disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Khodadoust MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE13009 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NPFHCDCQLLPLHRWLTGLNLRVGA---TCATPPNARGQRVKA-AAAVFEDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NPWACDCRARPLWAWFQ--RARVSSSDVTCATPPERQGRDLRALREADFQAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000WO-US32181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                     antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0444165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 91; DB Pred. No. 0.00 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8,
                                                                                                                                                                                  virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
0.00015;
                                                                                                                                                                                     analgesic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                        neuronal disorder;
                                                                                                                                                                                                                                       forensic biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48
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RESULT 7
AAG65808
ID AAG6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bone disorders such as osteoporosis, immune disorders such as rheumatoid arthritis, diabetes mellitus, cardiovascular disorders, liver disorders, viral diseases, pain or metabolic disorders. They are also useful as markers of disorders or disease states, or for precursors or markers for the predisposition of disease states. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a consensus human C-terminal leucine-rich repeat (LRRCT) domain. The LRR family member (referred as 31939) protein is useful for treating cell proliferative or differentiative disorder, e.g., cancer disorders or neuronal disorders, neurological disorders, demyelinating diseases such as multiple sclerosis, degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide useful for treating cancer, multiple sclerosis, Alzheimer's disease, osteoporosis, arthritis, and metabolic and liver disorders comprises the 31939 polypeptide belonging to the leucine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mapping, tissue typing, and forensic biology.
                                                                                                                                                                     04-OCT-2001.
                                                                                                                                                                                                   WO200172827-A2
                                                                                                                                                                                                                                                             antiinflammatory;
                                                                                                                                                                                                                                                                           LRR; leucine rich repeat; 33395; cytostatic; anti-HIV; antidiabetic; antiarthritic; neuroprotective; dermatological; immunosuppresive;
                                                                                                                                                                                                                                                                                                                          33395 LRR domain corresponding consensus amino acid
                                                                                                                                                                                                                                                                                                                                                          30-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                     AAG65808 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         such as Alzheimer's disease and Huntington's disease, spinocerebellar degenerations, disorders of the central or peripheral nervous system,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 3; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glucksmann
                                                                                                      24-MAR-2000;
                                                                                                                                     23-MAR-2001;
                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                       AAG65808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-662974/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-193919P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US10380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NPFNCDCELRWLLRWLRETNPRRLEDQEDLRCASPESLRGQPLLELLPSDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPWACDCRARPLWAWFQ----RARVSSSDVTCATPPERQGRDLRALREADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MILLENNIUM
                                                                        MILLENNIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                      2000US-191863P
                                                                                                                                      2001WO-US09470.
                                                                                                                                                                                                                                                                antiasthmatic;
                                                                         PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                     54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection assays such as chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 83; DB 22;
Pred. No. 0.0018;
                                                                                                                                                                                                                                                                                                                                                                                                                     AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                antiulcer;
                                                                                                                                                                                                                                                                antianaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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WPI; 2001-626254/72 Glucksmann MA;

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RESULT 8
AABD3603
ID AABC
XX
AC AABC
XX
DT 07-4
DT 07-1
CHUMP
KW CHUMP
KW CNS
KW Pros
KW Pros
KW Amyc

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNS disorder; central nervous system disorder; prostate disorder; prostate tisser disorder; prostate tisser disorder; prostate tisser prostate; benign prostatic hyperplasia; adenocarchoma; prostate cancer; genitourinary system carcinoma; testicular tumour; Alzheimer's disease; dementia; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; epilepsy; psychiatric disorder; mania; depression; schizophrenia; anxiety; phobic disorder; learning disorder; memory disorder; amnesia; migraine; protein protein interaction; cellular activity; neoplastic transformation; drug screening; forensic identification; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3335 polynucleotides and polypeptide can be used to prevent of treat disorders associated with 3335 expression, for example those involving aberrant cellular adhesion, proliferation or differentiation. Specific examples include meloblastoma, juvenile AIDS, diabetes mellitus, rheumatoid arthritis, systemic lupus erythematosis, multiple sclerosis, Chron's disease, ulcerative collities, asthma, anemia, and chronic active hapatitis. Sequences AAG65806-814 represent consensus amino acid sequences derived from a hidden Markov model corresponding to the LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide can be expressed
33395 polynucleotides ~~
                                                        New leucine-rich repeat-containing protein and nucleic acid molecules for diagnosing, treating neural disorders, such as neurodegenerative disorders, such as Alzhelmer's disease, dementia, epilepsy and prosta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide for preventing or treating disorders associated with cellular adhesion, proliferation or differentiation, comprises polypeptide 33395, a member of the leucine rich repeat protein family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE03603 standard; Protein; 54 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-2000; 2000WO-US33140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200142286-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leucine-rich repeat consensus #3
                                                                                                                                                                                                 WPI; 2001-381633/40
                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NPWACDCRARPLWAWFO --- -- RARVSSSDVTCATPPERQGRDLRALREADF 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention provides an isolated nucleic acid encoding a polypeptide he leucine rich repeat (LRR) family, designated 33395. The 33395 peptide can be expressed by standard recombinant methodology. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPFNCDCELRWLLRWLRETNPRRLEDQEDLRCASPESLRGQPLLELLPSDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leucine-rich repeat; LRR; AZAD; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     99US-0456592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 83;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2.
0.0018;
22;
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                                                               epilepsy and prostate
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ARESULT 9
AAE23805
ID AAE2
XX AAE2
XX TABLE
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DT 10-S
XX Memb
KW Memb
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders e.g. migraine. AZAD molecules are useful as markers of disorders or disease states, as markers for precursors of disease state, for predisposition of disease state or as markers of drug activity or pharmacogenomic profile of a subject. The AZAD polypeptide and polynucleotide are capable of modulating protein-protein interaction, e.g. by interacting with an extracellular component, thereby modulating ceilular activities, including attachment, adhesion, migration, patterning, growth and/or differentiation of a ceil. AZAD proteins regulate embryonic development and differentiation, tissue maintenance and function, pathological conditions, e.g. neuronal degeneration, neoplastic transformation and tumour progression. AZAD proteins are useful as immunogens to raise anti-AZAD antibodies which are useful to detect and isolate AZAD proteins and modulate its activity. AZAD
Membrane bound protein; secreted NOV protein; spermatogenesis; neoplasia; male infertility; anglogenesis; vascular pathology; orthopaedic disorder; inflammatory disease; congenital muscular dystrophy; muscular disorder; rheumatorid arthritis; fixed deformity; dysprothrombinaemia; cancer; arthrogryposis; hypoprothrombinaemia; hypokalaemic period paralysis; smith-Lemli-Opitz syndrome; carcinoid tumour; centrocytic lymphoma; hyperparathyroidism; Leigh syndrome; cervical carcinoma; leukaemia; hyperparathyroidism; Leigh syndrome; cervical carcinoma; leukaemia; mucular dystrophy; vitelliform type; McArdle disease; Meckel syndrome; multiple endocrine neoplasia I; multiple myeloma; hyperparathyroidism; parathyroid adenomatosis I; prolactinoma; digenic retinitis pigmentosa; somatotrophinoma; neovascular inflammatory vitreoretinopathy; arthritis; carcinoid syndrome; atopy; tendonitis; gene therapy; vaccine; LRRCT; leucine rich repeat C-terminal domain; fibromodulin-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epilepsy, psychiatric disorders e.g. depression, schizophrenic disorders, mania, anxiety or phobic disorders, learning or memory disorders e.g. annesia or age related memory loss, and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and cancer (e.g. adenocarcinoma, prostate cancer, genitourinary system carcinomas and testicular tumour). The neurodegenerative disorders include Alzheimer's disease, dementias related to Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosing AZAD-mediated or related disorders, which includes a neural disorder (e.g. neurodegenerative disorders, including CNS disorders) and a prostate disorder, e.g. prostatitis, benign prostatic hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secreted protein. AZAD polypeptide is useful for identifying a compound which modulates its activity
                                                                                                                                                                                                                                                                                                                                                                                                                         Fibromodulin-like (NOV5) protein conserved LRR C-terminal (LRRCT) domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE23805 standard; Protein; 54 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the AZAD protein are useful in gene therapy. AZAD sequences are also useful to map their respective genes on a chromosome, for tissue typing and in forensic identification of a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins are useful to screen for naturally occurring AZAD substrates and to screen for drugs or compounds which modulate AZAD activity. AZAD nuclaic acid fragments are useful as primers or hybridisation probes for the detection of AZAD-encoding nucleic acids. cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human AZAD protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZAD proteins and nucleic acid molecules are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 4; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPWACDCRARPLWAWFQ----RARVSSSDVTCATPPERQGRDLRALREADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPFNCDCELRWLLRWLRETNPRRLEDQEDLRCASPESLRGQPLLELLPSDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                esent sequence is a consensus sequence that homology with the C-terminal leucine-rich repeat sequence of AZAD protein which is a multiple leucine-rich repeat-containi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.2%;
35.3%;
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Pred. No. 0.0018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 54;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC invention are useful for treating or preventing NOV-associated disorders CC in humans and for manufacturing a medicament for treating a syndrome CC associated with human disease. They are useful for determining the CC presence of or predisposition to lung cancer. NOVI compounds are useful CC for development, differentiation and activation of thymic immune cells, CC pathologies related to spermatogenesis and male infertility, diagnosis CC of several human neoplasias and diseases or pathologies of cells in CC blood circulation such as red blood cells and platelets. NOVI nucleic cacids are useful for detecting specific cell types and as specific cC marker for cancers in tissues. NOV2 and NOV4 compounds are useful to CC direct the development of nervous system and angiogenesis and for CC compounds are useful for treating various orthopaedic disorders and/or CC injuries, inflammatory diseases of connective tissue e.g. rheumatoid CC arthritis, congenital muscular dystrophies, various muscular disorders, injuries, inflammatory diseases of connective tissue e.g. rheumatoid CC arthritis, congenital muscular dystrophies, various muscular disorders, CC useful for treating atopy, dysprothrombinaemia, hypoprothrombinaemia, CC useful for treating atopy, dysprothrombinaemia, hypoprothrombinaemia, cervical carcinoma, hypoprothrombinaemia, cuttopic syndrome, hypokalaemic period paralysis, acute promyelocytic leukaemia, NUMA/Raka type, macular dystrophy, viteliiform type, McArdle disease, tone of the control of control
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                            Matches
AAB82355;
                                                      AAB82355 standard; Protein; 54 AA
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is fibromodulin-like (NOV5) protein conserved leucine rich
repeat C-terminal (LRRCT) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            parathyroid adenomatosis 1, prolactinoma, hyperparathyroidism, carcinoid syndrome, digenic retinitis pigmentosa, somatotrophinoma, neovascular inflammatory vitreoretinopathy, arthritis and tendonitis. Sequences of the invention are also used in gene therapy and as vaccines. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type 2 Meckel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins and polynucleotides encoding such proteins. Sequences of the invention are useful for treating or preventing NOV-associated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel membrane bound and secreted NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel membrane bound and secreted NOV polypeptides, for treating, diagnosing and preventing male infertility, neurological, cardiac and vascular pathologies, and inflammatory diseases e.g. rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prayaga SK, Taupier RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-2000; 2000US-0689486
13-OCT-2000; 2000US-0687276
09-OCT-2001; 2001US-0973424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-OCT-2001; 2001WO-US31498
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                                                                                                                                                                                                                                                  1 NPWACDCRARPLWAWFQ----RARVSSSDVTCATPPERQGRDLRALREADF 47
                                                                                                                                                                                           NPENCDCELRWLLRWLREINPRRLEDQEDLRCASPESLRGQPLLELLPSDF
                                                                                                                                                                                                                                                                                                            1 Similarity
18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                       54 AA;
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                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          syndrome, multiple endocrine neoplasia I, multiple myeloma
                                                                                                                                                                                                                                                                                                                                29.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bandaru R;
                                                                                                                                                                                                                                                                                                         Score 83; DB 23;
Pred. No. 0.0018;
7; Mismatches 2:
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                                                                                                                                                                                                                                                                                                            Indels
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RESULT 11
AAG65814
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Best Local Similarity
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                                           LRR; leucine rich repeat; 33395; cytostatic; anti-HIV; antidiabetic; antiarthritic; neuroprotective; dermatological; immunosuppresive; antiinflammatory; antiasthmatic; antiulcer; antianaemic; hepatotropi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders, and for controlling cellular proliferative and/or differentiative disorders. JAFFA nucleic acids and proteins may be used to treat and/or diagnose a variety of immune disorders such as autoimmune disease and multiple sclerosis. JAFFA nucleic acids may also be used to express JAFFA protein, to detect JAFFA mRNA or a genetic alteration in a JAFFA gene, and to modulate JAFFA activity. Note: The present sequence is given in the Sequence Listing from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF90326) and polypeptides (see AAB82351). JAFFA is a novel member of the fibroblast growth factor family. JAFFA proteins may be useful for developing novel diagnostic and therapeutic agents for JAFFA-associated disorders such as cancers and ABO(H) blood group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated JAFFA nucleic acid molecules which encode novel fibroblast growth factor family members (JAFFA) are useful for developing novel diagnostic and therapeutic agents for JAFFA-associated disorders suc
                                                                                                                                                       30-JAN-2002
                                                                                                                                                                                          AAG65814;
                                                                                                                                                                                                                        AAG65814 standard; Protein; 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      described within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genetic alteration in a JAFFA gene, and to modulate JAFFA activity. Note: The present sequence is given in the Sequence Listing from the present invention, but does not correspond with the SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present
AAF90326) ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 132; 137pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-355881/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200138357-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JAFFA; human; fibroblast growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                             1 NPFNCDCELRWLLRWLREINPRRLEDGEDLRCASPESLRGGPLLELLPSDF
                                                                                                                                                                                                                                                                                                                                            1 NPWACDCRARPLWAWFQ----RARVSSSDVTCATPPERQGRDLRALREADF 47
                                                                                                                   domain corresponding consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listing as a consensus
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to human
                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
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                                                                                                                                                                                                                                                                                                                                                                                                  28.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 80; DB 22; Pred. No. 0.0044;
                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      It is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JAFFA polynucleotides (see
51). JAFFA is a novel memb
                                                                                                                     amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       described in the
                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                     acid
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 54;
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RESULT 12
AAU64229
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides an isolated nucleic acid encoding a polypeptide of the leucine rich repeat (LRR) family, designated 33395. The 3395 polypeptide can be expressed by standard recombinant methodology. The 3395 polynucleotides and polypeptide can be used to prevent or treat disorders associated with 3395 expression, for example those involving aberrant cellular adhesion, proliferation or differentiation. Specific examples include meloblastoma, juvenile AIDS, diabetes mellitus, rheumatoid arthritis, systemic lupus erythematosis, multiple sclerosis, chron's disease, ulcerative colltis, asthma, anemia, and chronic active hepatitis. Sequences Ad65806-814 represent consensus amino acid sequences derived from a hidden Markov model corresponding to the LRR domains of the the human 33395 polypeptide.
                              21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                          SAPHO syndrome; synovitis; acne: pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                          AAU64229 standard; Protein; 75 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide for preventing or treating disorders associated with cellular adhesion, proliferation or differentiation, comprises polypeptide 33395, a member of the leucine rich repeat protein family
                                                                                                                                                                                                                                                                                                                                                                          AAU64229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 3A-B; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glucksmann MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2001.
(CORI-) CORIXA CORP.
                                                                                               20-APR-2001; 2001WO-US12865.
                                                                                                                                 01-NOV-2001.
                                                                                                                                                               WO200181581-A2
                                                                                                                                                                                              Propionibacterium acnes
                                                                                                                                                                                                                                                                                                          Propionibacterium acnes immunogenic protein #25125
                                                                                                                                                                                                                                                                                                                                           27-FEB-2002
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16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 AA;
                              ; 2000US-199047P.
; 2000US-208841P.
; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73.5; DB Pred. No. 0.032;
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RESULT 13
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Best Local
                              21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis and ence) pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                        uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
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                                                                                                                                                                                                         Propionibacterium acnes
                                                                                                                                                                                                                                                                                             SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
                                                                                                                                                                                                                                                                                                                               Propionibacterium acnes immunogenic protein #26283
                                                                                                                                                                                                                                                                                                                                                                  27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU65387 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WTLPMRDLSLLTRSFRAETRLSRAPCQTNPERRSRDMKRRRICRYQA
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16; Conserv
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                             2000US-199047P.
2000US-208841P.
2000US-216747P.
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e J, Zhang Y,
                                                                                                   2001WO-US12865
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Pred. No. 1.4;
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RESULT 14
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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 N-PSDB;
                                                  Lombardi SJ,
                                                                               (USSA ) US SEC OF THE ARMY
                                                                                                                                                 29-MAR-1991;
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                                                                                                                                                                                                                    WO9116351-A
                                                                                                                                                                                                                                                   Nephila clavipes
                                                                                                                                                                                                                                                                                    Textiles; crystalline; tensile strength; SSP
                                                                                                                                                                                                                                                                                                                     Amorphous
                                                                                                                                                                                                                                                                                                                                                    30-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                    AAR14369 standard; Peptide; 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides. The proteins and their associated DNA sequences are use
the treatment, prevention and diagnosis of medical conditions caused
P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences AAU39105-AAU68017 represent Propionibacterium acnes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L'maisonneuve J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
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                 1991-339761/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WFCHGVLGARPHHVWFRR----TGSVRVAEPPHSDLPARVPGRGLRSLRD 73
AAQ15393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acne vulgaris
                                                                                                                                                                                                                                                                                                                   domain of spider silk protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID No 26582; 1069pp;
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/e J, Zhang Y,
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                                                Kaplan DL
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                                                                                                                 90US-0511114
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                                                                                                                                                                                                                                                                                                                                                    entry)
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Pred. No. 1.9;
4; Mismatches
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are used in
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant spider silk protein(s), for textiles - with modified relative and total amts. of crystalline and amorphous domains, for improved commercial properties, e.g tensile stren
                                                                                                                                                                                                          Prostate cancer associated gene sequences, cancer antigens, useful for treatment, prev
                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastrointestimal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate cancer antigen protein sequence SEQ ID NO:977.
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                                                                                                                             Claim 11; Page 1417;
                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA,
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11; Conser
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ROSEN C A.
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                                                                                                                                                                                                                                                                                                                                                                                  SM;
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                                                                                                                             2338pp; English
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proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal,

AAF15566 to AAF16505 encode the human prostate cancer associated

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Search completed: April 4, 2003, 08:23:48 Job time: 44.963 secs
                                                                                                                                                                                                                                                                         Ouery Match 20.1%; Score 57; DB 21; Length 59; Best Local Similarity 43.5%; Pred. No. 4.9; Matches 10; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
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re greater than or equal to the score of the result being printed,
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/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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Sequence 976, App
Sequence 179, App
Sequence 1086, Ap
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US-09-864-761-33329	US-09-731-872-476	115-09-764-872-380	115-09-864-761-37930	US-10-056-407-20	US-09-864-761-33699	US-09-793-306-25	US-09-023-588-25	US-09-073-009-25	US-09-925-300-1048	US-09-764-869-1177	US-10-091-504-1177	US-09-764-869-799	US-10-091-504-799	US-09-867-550-336	US-10-102-806-465	US-09-867-550-738	US-09-764-847-565	US-10-092-154-565	US-09-847-102A-136	US-09-867-550-936	US-09-864-761-43837	US-09-864-761-36140	US-09-772-719-50	US-09-967-237-50	US-10-228-806-44
Sequence 33329, A	Sequence 300, App	add 085 Samples	Sequence 37930. A	Sequence 20 Appl	Sequence 33699, A	Sequence 25, Appl	Sequence 25, Appl	Sequence 25, Appl	Sequence 1048, Ap	Sequence 1177, Ap	Sequence 1177, Ap	Sequence 799, App	Sequence 799, App	Sequence 336, App	Sequence 465, App	Sequence 738, App	Sequence 565, App	Sequence 565, App	Sequence 136, App	Sequence 936, App	Sequence 43837, A	Sequence 36140, A	Sequence 50, Appl	Sequence 50, Appl	Sequence 44, Appl

ALIGNMENTS

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FEATURE:

NAME/KEY: misc_feature

LOCATION: (48)

OTHER INFORMATION: Xaa ee

NAME/KEY: misc_feature

LOCATION: (51)

OTHER INFORMATION: Xaa ee

NAME/KEY: misc_feature

LOCATION: (66)

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Sequence 976, Application US/10091504
Publication No. US20030059908A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/091,504
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2442
Prior Application removed - See File Wrapper or Palm SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 976
LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen et al. TITLE OF INVENTION: NUC FILE REFERENCE: PC007C1
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TYPE: PRT
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62 FLWG
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE ; LOCATION: (66) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-869-976
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LENGTH: 77
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Matches 21
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                                                                       Matches
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CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
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NAME/KEY: SITE
LOCATION: (48)
OTHER INFORMATION: X
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CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: PZC
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                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens US-09-764-869-1086
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US-10-091-504-1086
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; LENGTH: 68
; TYPE: PRT
                                                                                                   GENERAL INFORMATION: APPLICANT: Leach, M
                                                                                                                                          Sequence 1320, Application US/09867550 Patent No. US20020082206A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prior Application removed - SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1086
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOO7
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442 SOFTWARE: PatentIn Ver. 2.0
                           APPLICANT:
                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC007C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells a
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TYPE: PRT
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Local Similarity 35.2%;
les 19; Conservation
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Conley, Pamela
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Pred. No. 9.
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Best Local Similarity
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Best Local Similarity
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PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1320
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
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NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FRANCEQ for Windows Version 4.0
SEQ ID NO 2044
                                                                                                                                                                                                                                LENGTH: 98
                                                                                                                                                                                                                                                                                                                                    URRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
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NAME/KEY: VARIANT
LOCATION: (5)
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OTHER INFORMATION: Wherein Xam may be any one of Ala or Arg
OTHER INFORMATION: Leu or Lys or Pro or Ser or Thr or Val
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ORGANISM: Homo sapiens
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PRAWTRPALPLCLSARRSMMMQMRRA---PMSDDILARDRGSRLSRGNRRNGGGGCRDDD
                            PAAPTRPGSRARGNSSSNHLYGVAEAGAPPADPSTLYRDLPAEDSRG--RQGGDAPTEDD
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Conley, Pamela
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ban, Fuad,
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Pred. No. 77;
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Pred. No.
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SEQ ID NO 39016
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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OTHER
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ORGANISM: Homo
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PRIOR FILING DATE: 2001-01-30
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                                                                                             OTHER INFORMATION:
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PRIOR FILING DATE: 2000-08-03
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CURRENT FILING DATE: 2001-05-23
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Hanzel, David K.
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N: EXPRESSED IN ADULT LIVER, SIGNAL = 14

N: EXPRESSED IN PLACENTA, SIGNAL = 16

N: EXPRESSED IN LUNG, SIGNAL = 16

N: EXPRESSED IN HEART, SIGNAL = 14

N: EXPRESSED IN HELA, SIGNAL = 17

N: EXPRESSED IN HELA, SIGNAL = 13

N: EXPRESSED IN FETAL SIGNAL = 14

N: EXPRESSED IN FORD SIGNAL = 14

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N: EXPRESSED IN BONE MARROW, SIGNAL = 14

N: SWISSPROT HIT: P14378, EVALUE 5.90e+00

N: EST_HUMAN HIT: BE278817.1, EVALUE 5.50e+00
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                                                                                  RESULT 10
US-09-073-009-23
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Patent No. US20010012888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                       Patent No. US20010012888A1 GENERAL INFORMATION:
                                                                                                                                                                                                                           Query Match
                                                                     Sequence 23,
                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 206-682-6031
NFORMATION FOR SEQ ID NO:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 PAAGTPSAPGSRTPGNPAT----AVSGTPAPPA 81
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SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PAA--PTRPGSRARGNSSSNHLYGVAEAGAPPA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 05-MAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                          19
                                                                                                                                                                  25 AEAGAPPADPSTLYRDLPAEDSRGRQGGDAPTEDDYWGGYGGEDQRGEQMCPGAACQ 81
                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                        AQAGLLEAEHQAIIRDV------SAACQ 51
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                    94 amino acids
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                                                                     Application US/09073009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6300 Coumbia Center, 701 Fifth Ave
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Skeiky, Yasir A.W.
 Alderson, Mark
Dillon, Davin C
Skeiky, Yasir A
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                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEED and BERRY
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 Davin C.
Yasir A.W.
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                                                                                                                                                                                                  Score 55; DB : Pred. No. le+0: 5; Mismatches
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Pred. No.
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US-09-073-009-31
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application US/09073009 Patent No. US20010012888A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 144
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Maki, David J.
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MEDIUM TYPE: Floppy disk
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                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: FR PC PC POS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                           APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antor
TITLE OF INVENTION: COMPOUNDS
                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                             SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 AQAGLLEAEHQAIIRDV-----
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hes 16; Conser
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STRANDEDNESS: sir
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                                                                                                                                                                             STATE: Washington
                                                                                                                                                                                              CITY: Seattle
CLASSIFICATION:
               FILING DATE:
                                                                                                                                                              COUNTRY:
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                                APPLICATION NUMBER:
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SYSTEM: PC-DOS/MS-DOS
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             UMBER: US/09/073,009
.05-MAY-1998
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Pred. No. le+02;
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US-09-023-588-21
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US-09-023-588-21
 Query Match
Best Local Similarity
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Rest Local Similarity 28.1
atches 16; Conservative
                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                     TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 206-622-490
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                             ORIGINAL SOURCE:
                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark R.
TITLE OF INVENTION: METHOD FOR THE ISOLATION OF NOVEL ANTIGENS
UNMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 14-FEB CLASSIFICATION:
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                                                                                                              TOPOLOGY:
                                                                                                                                                       ENGTH:
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TYPE: amino acid
STRANDEDNESS: single
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                                                            Mycobacterium tuberculosis
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Score 55;
Pred. No.
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Pred. No. 1e+02;
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           Length 94;
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                                                                                                                                  Sequence 31, Application US/09023588 Patent No. US20020081579A1 GENERAL INFORMATION:
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US-09-023-588-23
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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 CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                            APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark R.
TITLE OF INVENTION: METHOD FOR THE ISOLATION OF NOVEL ANTIGENS
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Myc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,588
FILING DATE: 14-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark R.
                                                                                                                                                                                                                                         19 AQAGLLEAEHQAIIRDV------SAACQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                        25 AEAGAPPADPSTLYRDLPAEDSRGRQGGDAPTEDDYWGGYGGEDQRGEQMCPGAACQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SEED and BERGE . 701 Fifth Avenue STREET: 5300 Columbia Center, 701 Fifth Avenue
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WENTION: METHOD FOR THE ISOLATION OF NOVEL ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis
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28.1%;
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Pred. No. 1e+02;
5; Mismatches 12;
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701 Fifth Avenue
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com

CITY: Seattle STATE: Washington

COUNTRY:

98104

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APPLICANT: Jen, Shyian
APPLICANT: Lodes, Michael
APPLICANT: Lodes, Michael
APPLICANT: Corixa Corporation
YETTLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
YETLE OF INVENTION: Of Tuberculosis
FILE REFERENCE: 014058-008740US
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 94
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide ORIGINAL SOURCE: ORGANISM: Mycobacteri US-09-023-588-31
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US-09-793-306-21
                                                                                 ; OTHER INFORMATION: Tb398 ORF-2 US-09-793-306-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.6%;
Best Local Similarity 28.1%;
Matches 16; Conservative
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NAME: Maki, David J.

NAME: Maki, David J.

REGISTRATION UNMBER: 2101

TELEPROMUNICATION: INFORMATION:

TELEPRONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 94 amino acids
Query Match 11.6%; Score 55; DB 10
Best Local Similarity 28.1%; Pred. No. 1e+02;
Matches 16; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Campos-Neto, Antonio APPLICANT: Skeiky, Yasir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                               FEATURE:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 14-FE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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Ovendale, Pamela
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linear
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                                                DB 10; Length 94;
               12;
               Indels
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Search completed: April 4, 2003, 08:31:57 Job time : 146.444 secs

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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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length: 100
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/18a/5B_COMB.pep:*
/cgn2_6/ptodata/1/18a/6B_COMB.pep:*
/cgn2_6/ptodata/1/18a/6B_COMB.pep:*
/cgn2_6/ptodata/1/18a/6B_COMB.pep:*
/cgn2_6/ptodata/1/18a/PCTUS_COMB.pep:*
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US-09-314-268-138
US-09-787-739-50
US-09-178-115-50
US-09-177-776-50
US-09-177-750A-50
US-08-477-50A-50
US-08-486-756A-50
US-08-485-862B-50
US-08-485-863A-50
US-08-485-0450-50
US-08-485-0450-50
US-08-485-0450-50
US-08-475-411A-113
US-08-475-411A-113
US-08-475-411A-112
US-08-475-411A-115
US-08-478-029A-115
US-08-478-029A-115
US-08-478-029A-115
US-08-478-029A-115
US-08-478-029A-115
US-08-475-411A-115
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    Sequence
   138, Appl
50, Appl
113, App
113, App
112, App
112, Appl
112, Appl
113, Appl
115, Appl
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US-09-314-268-138
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46.5	46.5	47	47	47	47	47	47	47	47.5	48	48	48	48.5	48.5	48.5	48.5	49.5
9.8	9.8	9.9	9.9	9.9	9.9	9.9	9.9	9.9	10.0	10.1	10.1	10.1	10.2	10.2	10.2	10.2	10.4
76	76	85	85	70	67	58	56	53	50	73	68	56	98	98	82	60	86
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US-09-218-950-53	US-08-284-391B-53	US-08-478-029A-114	US-08-475-411A-114	US-09-314-268-141	US-08-897-924A-8	US-08-897-924A-9	US-08-850-910A-24	US-08-897-924A-10	US-09-314-268-159	US-09-564-805-213	US-09-220-528-50	US-08-897-924A-2	US-08-665-202-38	US-08-211-202-111	US-07-609-716-114	US-09-336-536-13	US-08-343-443B-7
	Sequence 53, Appl	Sequence 114, App	Sequence 114, App	Sequence 141, App	Sequence 8, Appl1	9	24,	Sequence 10, Appl	Sequence 159, App	Sequence 213, App	Sequence 50, Appl	Sequence 2, Appli	Sequence 38, Appl	Sequence 111, App	Sequence 114, App	Sequence 13, Appl	Sequence 7, Appli

ALIGNMENTS

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Sequence 138, Application US/09314268
; Sequence 138, Application US/09314268
; Patent No. 6346377
; GENERAL INFORMATION:
   APPLICANT: DOORDAY, JOHN
   TITLE OF INVENTION: IMPROVEMENTS IN OR RELAT
   TITLE OF INVENTION: VIRUSES
; FILE REFERENCE: 3789/80902
; CURRENT APPLICATION NUMBER: US/09/314,268
; CURRENT FILING DATE: 1999-03-19
; EARLIER APPLICATION NOWHER: 09/314,268
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 138
; LENGTH: 87
; TYPE: PAT
; ORGANISM: Human papillomavirus type 47
US-09-314-268-138
                                                                                                                                                                                      ; Sequence 50, Application US/08787739
Patent No. 6027887
; GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Pr
NUMBER OF SEQUENCES: 96
                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-08-787-739-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                        STREET: 369 Pine Str
CITY: San Francisco
STATE: California
                                                                                                                                ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, S
                                                                                                                                                                                                                                                                                                                                                                                                                         29 PPPPPTGPGLR-----RSTRLVLVPGQGPPP-----DLPAPPVEGEVEGHPQGKD
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20; Conserv
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IBM PC compatible
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Pred. No. 14;
1; Mismatches
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; DESCRIPTION:
US-08-787-739-50
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Best Local Similarity 39.5%;
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                                                                                                                                                                                                                                                                                                           Patent No.
EARLIER
EARLIER
                                                                 EARLIER APPLICATION NUMBER: 08/787,739
EARLIER FILING DATE: 1997-01-24
EARLIER APPLICATION NUMBER: 08/485,049
EARLIER FILING DATE: 1995-06-07
                                                                                                                                                                                                      TITLE OF INVENTION: MN Gene and Protein FILE REFERENCE: D-0021.5A
                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                      EARLIER
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                                                                                                                                                                        CURRENT
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INFORMATION FOR SEQ ID NO:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Lauder, Leona L. REGISTRATION NUMBER: 3
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                               APPLICATION NUMBER: 08/486,756 FILING DATE: 1995-06-07
                                                                                                                                   APPLICATION NUMBER: US/09/178,115
FILING DATE: 1998-10-23
APPLICATION NUMBER: 09/177,776
FILING DATE: 1998-10-23
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o. 6297041
APPLICATION FILING DATE:
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MN protein proteoglycan-like region
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07-JUN-1995
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            NUMBER: 08/477,504
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Pred. No. 34;
5; Mismatches
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; LENGTH: 59
; TYPE: PRT
; ORGANISM: HUMAN
US-09-178-115-50
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Best Local
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LENGTH: 59
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NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
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EARLIER FILING DATE: 1992-10-21
EARLIER APPLICATION NUMBER: PV-709-92
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                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/177,776A CURRENT FILING DATE: 1998-10-23 EARLIER APPLICATION NUMBER: 08/787,739 EARLIER FILING DATE: 1997-01-24
                                                              EARLIER FILING DATE: 1992-10-21
EARLIER APPLICATION NUMBER: PV-709-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MN Gene and Protein FILE REFERENCE: D-0021.5A
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               SOFTWARE:
                              NUMBER OF SEQ ID NOS: 116
                                              EARLIER FILING DATE: 1992-03-11
                                                                                               EARLIER APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pastorek,
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ID NO
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                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                FILING DATE:
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1995-06-07
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1995-06-07
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Pred. No.
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US-08-477-504A-50

US-98-477-504A-50

; Sequence 50, Application US/08477504A

; Patent No. 5972353

; GENERAL INFORMATION:
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US-08-481-658B-50
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GENERAL INFORMATION:
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                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
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ORGANISM: HUMAN
                                                                                                                                                                                                                                                       MOLECULE TYPE:
DESCRIPTION:
DESCRIPTION:
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APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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Local Similarity 39.5%;
nes 15; Conservative
                                                                                                                27 DLPSEE-----
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                                                                                                                                                                             Local Similarity
nes 15; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: California
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TYPE: amino acid
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Region of homology to collagen alpha
l chain
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                                                                                                                DSPREED---PPGEEDLPGEEDLPG
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                                                                                                                                                                           Score 54; DB
Pred. No. 61;
5; Mismatches
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Pred. No. 34;
                                                                                                                                                                                       DB 61;
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RESULT 7
US-08-486-756A-50
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; DESCRIPTION:
US-08-477-504A-50
                                                                                                                                                                                                                                                                                                                       Sequence 50, Application US/08486756A Patent No. 5981711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: MN Gene and Protein
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                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 39.9 nes 15; Conservative
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CITY: Tiburon
                                                                                                                 COUNTRY:
                                                                                                                                        STATE:
                                                                                                                                                    CITY: Tiburon
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                                                                                                                                                                  6 Mariposa Court
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6 Mariposa Court
                                                                                                                    USA
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                                                                                                                                                                                      Leona L.
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Region of homology to collagen alpha
1 chain
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                 Version #1.30 (EPO)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DESCRIPTION:
DESCRIPTION:
08-486-756A-50
                                  NFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION NUMBER: US 08/260,190
PTILING DATE: 15-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-35-2034
                                                                                                                                                                                     FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
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ATTORNEY/AGENT INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                    FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                     NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-
                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/485,862B
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Region of homology to collagen alpha
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Pred. No. 61;
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                                                      Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
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DESCRIPTION:
DESCRIPTION:
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STREET:
CITY: Tiburon
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                         TOPOLOGY: 1. MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-UN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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APPLICANT: Pastorekova, Silvia
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                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/487,077A FILING DATE: 07-JUN-1995
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27 DLPSEE---
                          40 DLPAEDSRGRQGGDAPTEDDYWGGYGGEDQRGEQMCPG
                                                                                                                             DESCRIPTION:
                                                                                                                                                                                                                                                                                                   NAME: Lauder, Leona L. REGISTRATION NUMBER: 3
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les 15; Conserv
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                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                             Region of homology to collagen alpha 1 chain
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-DSPREED---PPGEEDLPGEEDLPG 54
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                                                                     11.4%;
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                                                        Score 54; DB Pred. No. 61; 5; Mismatches
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Pred. No.
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image: Mismatches
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                                                        Gaps
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RESULT 10 US-08-485-863A-50

Sequence 50 Patent No.

50, Application US/08485863A o. 6093548

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US-08-485-049D-50 
; Sequence 50, Ap
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Best Local Similarity 39.
                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                 TITLE OF INVENTION: MN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
Pastorek, Jaromir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/JOCKET NUMBER: D-0021.36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/01
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
STREET:
CITY: Tiburon
CITY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                             STREET: 369 Pine SCITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FITLE OF INVENTION:
                                                          COUNTRY: U
                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                            40 DLPAEDSRGRQGGDAPTEDDYWGGYGGEDQRGEQMCPG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION: Region of homology to collagen alpha DESCRIPTION: Region of homology to collagen alpha DESCRIPTION: 1 chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                                                                                                                                                                       ), Application US/08485049D 6204370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                  E: Leona L. Lauder
369 Pine Street
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                                                                       USA
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VENTION: MN Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leona L.
                                                                                                                                                                                   MN Gene and Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              8
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Patent No. 5514581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 9
                                                                                  APPLICATION NUMBER: US/07/609
APPLICATION: 06-NOV-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BETTCAM I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-55
TELECOMMUNICATION INFORMATION:
TELEPAN: 415-398-3249
                                                                    TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
APPLICATION TO NUMBER: 15-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                               SEQUENCE CHARACTERISTICS: LENGTH: 72 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
DESCRIPTION: Region of homology to collagen alpha
DESCRIPTION: 1 chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ferrari, Franco A. APPLICANT: Cappello, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,049D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DÂTE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Four Embarca
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UZIP: 94111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                   amino acid
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single
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39.5%;
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Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Test, Albritton & Herbert
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; TOPOLOGY: 1i ; MOLECULE TYPE: US-07-609-716-113

peptide

Query Match

DB 1;

Length

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
Best Local Similarity
                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-475-411A-113
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tent No. 6140072
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                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ferrari, APPLICANT: Cappello,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 09-NOV-1988
PRIOR APPLICATION UNMER: US 07/114,618
FILING DATE: 29-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 01
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NUMBER: TECCHICAL PROPERTY OF THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PPAAPTRPGSRARGNSSSNHLYGVAEAGAPPADPSTLYRDLPAEDSRGRQG--GDAPTED 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/609,716 FILING DATE: 06-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-9/RFT/MTK
                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Trecartin, Richard F.
                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94111
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                                                                                                                                                                                                                                            : 72 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Flehr, Hohbach, Test, Albritton & Herbert Four Embarcadero Center, Suite 3400
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                                                                                                                                                                           linear
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09-NOV-1988
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Synthetic Protein Polymer
119
   11.3%;
26.1%;
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Pred. No. 48;
          Score 53.5; DB 4; pred. No. 48;
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                                           Length 72;
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US-08-478-029A-113
В
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Best Local Sim
Matches 24;
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/478,029A FILING DATE: 07-UN-1995 CLASSIFICATION: 435
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MEDIUM TYPE: Floppy (
COMPUTER: IBM PC comp
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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NAME: Trecartin, Richard F.
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
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APPLICATION NUMBER:
                                                                                                                                   MOLECULE TYPE:
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/609,716 FILING DATE: 06-NOV-1990
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                                                                                                                                                                                              LENGTH:
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                            1 PPAAPTRPGSRARGNSSSNHLYGVAEAGAPPADPSTLYRDLPAEDSRGRQG--GDAPTED 58
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                                                             Similarity 26. 24; Conservative
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                                                                                                                                                                                                 72 amino acids
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                                                                                                                                                     linear
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                                                                            Score 53.5;
Pred. No. 48;
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STATE: COUNTRY: COUNTRY: SAII

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/07/609,716
FILING DATE: 06-NOV-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
AAME: ROWLAND, 8Ertram I
REGISTRATION NUMBER: 20015
REFERRATION NUMBER: A-55186-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
INFORMATION FOR SEQ ID NO: 1112:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
TYPE: mamino acids
STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: peptide
US-07-609-716-112
Search completed: April 4, 2003, 08:26:07 Job time: 23.6667 secs
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US-07-609-716-112
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Patent No. 5514581
GENERAL INFORMATION:
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APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                            40 ----GPKGDGSPGPAVCEPGYIGSRCDAGP 65
                                                                                                                   59 DYWGGYGGEDORGEOMCP----GAACQAPP 84
                                                                                                                                                      1 PPAAPTRPGSRARGNSSSNHLYGVAEAGAPPADPSTLYRDLPAEDSRGROG--GDAPTED 58
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CITY: San Francisco
STATE: CA
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Perfect score:
Sequence:
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Maximum DB
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length: 100
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Listing first 45 s
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  GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.
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                        Q9q0d8 herpes simp
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Q15215 homo sapien
Q15905 homo sapien
Q05200 homo sapien
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Q53824 mycobacteri
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Q9q0d4
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herpes simp
herpes simp
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Q67789 human adeno		92		51.5	5
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		69		51.5	3
Q92kb9 rhizobium m		56		51.5	2
Q9eun9 corynebact		95	10.9	52	11
Q24703 drosophila		87	•	52	0
Q9vps9 drosophila		99	•	52.5	39
P73629 synecho		90		52.5	38
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Q9pvq3 oryzias lat		98		53	5
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Q91413 notophthalm	13 Q91413	89		53	ພ
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Q9vrk7 drosophila	o	91		53.5	27
Q65541 bovine her		53		53.5	26
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Matches 22
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Liljeqvist J.A., Svennerholm B., Bergstrom T.;
"Conservation of type-specific B-cell epitopes of glycoprotein G in
clinical herpes simplex virus type 2 isolates.";
J. Clin. Microbiol. 38.4517-4522(2000).
                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Glycoprotein G-2 (Fragment).
                                                                                                                                                SEQUENCE
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Interpro; IPR003363; Herpes_gG.
Pfam; PF02400; Herpes_gG; 1.
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
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49
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nes 22; Conserv
                       62 GGYGGEDQRGEQMCPGAACQAP 83
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GAGDGEPPEDDDSATGLAFRTP
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                                              ATPGTRGTARTPPTDPKTHPHGPAD -- APPGSPAP -- -- -- PPPEHRGR -- -- -- PEEFE 48
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7130 MW;
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Pred. No. 31;
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Best Local Similarity
                                                                                                                                                                                                                                                           0900D6;
01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, Glycoprotein G-2 (Fragment).
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01-JUN-2002
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01-MAY-2000
                                            NON_TER
                                                                                          MEDLINE-20553357; PubMed-11101589; Liljeqvist J.A., Svennerholm B., Bergstrom T.; Liljeqvist J.A., Svennerholm B., Bergstrom T.; "Conservation of type-specific B-cell epitopes of clinical herpes simplex virus type 2 isolates."; J. Clin. Microbiol. 38:4517-4522(2000).

EMBL; AJ270567; CAB58430.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liljeqvist J.A., Svennerholm B., Bergstrom T.; Conservation of type-specific B-cell epitopes clinical herpes simplex virus type 2 isolates. J. Clin. Microbiol. 38:4517-4522(2000).
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Alphaherpesvirinae; Sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9Q0D7
                                                                      Pfam; PF02400;
                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=VI-448;
                                                                                                                                                                                                    Alphaherpesvirinae; Simplexvirus NCBI_TaxID=10310;
                                                                                                                                                                                                                          Herpes simplex virus (type 2).
Viruses: dsDNA viruses, no RNA stage;
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STRAIN-VI-449;
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 Similarity
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2400; Herpes_gG; 1.
                                                                       IPR003363; Herpes_gG.
2400; Herpes_gG; 1.
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70 AA;
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(TIEMBLrel. 21, Last annotation updat)
1 G-2 (Fragment).
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AA;
                                                                      Herpes_gG;
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  13
26
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Last sequence up
Last annotation
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Pred. No. 31;
  Score
Pred.
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                                    051CA419B1A5440F CRC64;
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  62.5;
No. 31;
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Q9Q0D5;
01-MAY-2000 (TrEMBLrel. 13, Cr
r 01-MAY-2000 (TrEMBLrel. 21, L
r 01-JUN-2002 (TrEMBLrel. 21, L
71"\caparotein G-2 (Fragment).
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Best Local :
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Q9Q0D0;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-JUN-2002 (TrEMBLrel. 21, L
Glycoprotein G-2 (Fragment).
clinical
J. Clin.
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SEQUENCE
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"Conservation of type-specific B-cerystrom Clinical herpes simplex virus type 2 isolates."
J. Clin. Microbiol. 38:4517-4522(2000).
J. Clin. Microbiol. 38:4517-4522(2000).
                                                                                                                                                                                     Alphaherpesvirinae;
NCBI_TaxID=10310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003363; Herpes_gG.
Pfam; PF02400; Herpes_gG; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herpes simplex virus (type 2).
Viruses; dsDNA viruses, no RNA stage;
  Liljeqvist J.A., Svennerholm B., Bergstrom T.; "Conservation of type-specific B-cell epitopes clinical herpes simplex virus type 2 isolates." J. Clin. Microbiol. 38:4517-4522(2000).
                                                                                          STRAIN=VI-1070;
MEDLINE=20553357; PubMed=11101589;
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      Herpes simplex virus (type 2).
Viruses; dsDNA viruses, no RNA
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Last annotation updat
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Pred. No. 3
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RESULT 6
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Best Local :
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Best Local S
Matches 18
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                                                                                                                                                      096TS2;
096TS2;
01-DEC-2001
01-DEC-2001
01-MAR-2002
Fowler T.J., Mitton M.F., Vaillancourt L.J., Raper C.A.; "Changes in mate recognition through alterations of pheromones receptors in the multisexual mushroom fungus Schizophyllum communitied (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                      SEQUENCE FROM N.A.
STRAIN-4-8;
                                                                                         Schlzophyllum commune (Bracket fungus).
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Schlzophyllaceae; Schlzophyllum.
                                                                                                                                                                                                                                                                                                                                                 NON_TER
SEQUENCE
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Q9Q0C9;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                  "Conservation of type-specific B-cell epitopes clinical herpes simplex virus type 2 isolates."
J. Clin. Microbiol. 38:4517-4522(2000).
EMBL; AJ270574; CAB58437.1;
InterPro: IPR003363; Herpes_gG.
                                                                                                                   Schizophyllum commune
                                                                                                                                                                                                                                                                                                                                                                       NON_TER
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Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Simplexvirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10310;
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InterPro; IPR003363; Herpes
Pfam; PF02400; Herpes_gG; 1
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18; Conservative
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7091 MW;
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    Last sequence update)
    Last annotation updat
precursor Bbp2-5.

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                                                                                                                                                                                                                                                                                                            Score 61;
Pred. No.
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                                                                                                                                                                                               PRT;
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Q15905;
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O1-NOV-1996 (TrEMBLrel. C
O1-DEC-2001 (TrEMBLrel. I
YB-1 protein.
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Best Local S
               SEQUENCE FROM N.A.
MEDLING=96226173; PubMed=8657568;
MAKINO Y., Ohga T., Toh S., Koilke
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Q15215
Q15215;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (Trembled in 1 (Fragment)
   Kohno
                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                     YB-1
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MEDLINE=84298176; PubMed=6089212;
Azen E.A., Lyons K.M., McGonigal T.,
Maeda N., Vanin E.F., Carlson D.M.,
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InterPro; IPR001230; Prenyl_site.
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SEQUENCE 92 AA; 9594 MW; A3CBD180AB379C03
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20; Conservative
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6; AAA36503.1; -.
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Catarrhini; Hominidae;
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Q05200;
Q1-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, I
01-DEC-2001 (TrEMBLrel. 19, I
C-Ha-ras protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases EMBL; X96666; CAA65446.1; - SEQUENCE 74 AA; 7123 MW; 7BF1BEDEF4ECE559 CRC64;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2002 (TrEMBLrel. 21,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Steiner
                                                                                                                                      Homo sapiens (Human).
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Biol. (Mosk.) 23:491-
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CAA36265.1;
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uth K., Skriner
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pred. No. 6
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Last annotation update)
hnRNP homolog (Fragments).
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"purification and partial sequencing of the nuclear aut
shows that it is indistinguishable from the A2 protein
heterogeneous nuclear ribonucleoprotein complex.";
J. Clin. Invest. 90:1061-1066(1992).
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01-NOV-1996
01-DEC-2001
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                   053824;
053824;
01-JUN-1998
01-JUN-1998
01-MAR-2002
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MEDILINE=96067614; PubMed=7487954;

Chiodo A.A., Sillence D.O., Cole W.G., Bateman J.F.;

"Abnormal type III collagen produced by an exon-17-skipping of the COL3Al gene in Ehlers-Danlos syndrome type IV is not incorporated into the extracellular matrix.";

Biochem. J. 311:939-943(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                           IN--GSPGGKGEMGPAGIPGAPGLMGARGPP
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Pro; IPR000087; Collagen.
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PS00030; RRM_RNP_1; UNKNOWN_1.
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8 (TrEMBLrel. 06, L;
2 (TrEMBLrel. 20, L;
31 protein Rv0810c.
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68
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Pred. No.
6; Mismatch
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Best Local
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RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher G., Harris E.

RA Gordon S.V., Eiglmeler K., Gas S., Barry C.E. III, Tekaia F.,

RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.

RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

RA Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,

RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                 MEDLINE-2053337; pubMed=11101589;
Liljeqvist J.A., Svennerholm B., Bergstrom T.;
"Conservation of type-specific B-cell epitopes of glycoprotein clinical herpes simplex virus type 2 isolates.";
J. Clin. Microbiol. 38:4517-4522(2000).
EMBL, AJ70569; CAB58432.1;
InterPro: IR003363; Herpes_gG.
Pfam: PF02400; Herpes_gG; 1.
Pfam; PF02400; Herpes_gG;
NON_TER 1 1
NON_TER 70 70
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01-MAY-2000
01-JUN-2002
                                                                                                                                                                                      Alphaherpesvirinae;
NCBI_TaxID=10310;
                                                                                                                                                                                                           Herpes simplex virus (type 2).
Viruses; dsDNA viruses, no RNA stage;
                                                                                                                                                         SEQUENCE FROM N.A.
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Hypothetical protein; Complete
SEQUENCE 60 AA; 6900 MW; 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               laboratory strains.";
Submitted (APR-2001) to the
EMBL; AL022004; CAA17616.1;
EMBL; AE006973; AAK45073.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula
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                                                                                                                                                                                                                                                      1 MAY-2000 (TrEMBLrel 13, 1-MAY-2000 (TrEMBLrel 13, 1-JUN-2002 (TrEMBLrel 21, 1) (Tremburel 6-2 (Fragment))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria
Actinomycetales; Corynebacterineae;
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"Conservation of type-specific B-cell epitopes o
clinical herpes simplex virus type 2 isolates.";
J. Clin. Microbiol. 38:4517-4522(2000).
EMBL; AJ270570; CAB58433.1;
InterPro; IPR003363; Herpes_gG.
Pfam; PF02400; Herpes_gG; 1.
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0900D3;
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MEDLINE=20553357; PubMed=11101589;
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Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Simplexvirus.
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completed: April ne : 69.1111 secs
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                                                                                                                      3 AAP-TRPGSRARGNSSSNHLYGVAEA-GAPPADPSTLYRDLPAEDSRGRQGGDAPTEDD 59
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Pred. No. 1.2e+02;
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ES64_MYCTU
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ES61_MYCTU
UV15_SCHPO
ES66_MYCTU
NEU1_ANSAN
PRP5_HUMAN
QRP7_DAUCA
VE4_HPV28
GATC_DEIRA
NIFU_FRAALL
RUBR_CHLLT
S6B2_YEAST
YIFL_ECOLI
DSS1_HUMAN
Y898_HUMAN
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Y898_HUMAN
           PSAC_PINTH
ANX7_BOVIN
PEP2_THUTO
TRBK_AGRTU
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RESULT 2
CALC_BOVIN
ID CAIC_BOVIN STANDARD; PRT; 86 AA.
AC P25508;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Collagen alpha 1(XII) chain (Fragments).
GN COLL2A1.
OS Bos taurus (Bovine).

update)

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GYGGE-DQRGEQMCPGAACQAPP 84 AEGAEGEEKAEEPAPGATADDAP

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GSRARGNS	imilarity Conserv	S0568 ion. 1 20 49 73 5 AA;	255:149-153 255:149-153 DN: CELLULAR RITY: TO 87	0.0	52; D.,	nta; Metazoa; .a; Eutheria; xID=10116;	01-FEB-1991 (Rel. 01-FEB-1991 (Rel. 01-FEB-1991 (Rel. 01-FEB-1991 (Rel. Protein kinase C s	STA		8
SSSNHLYG	13.3% 30.1% vative	1, 1 21 50 74 7593 MW;	.0) 255:149-153(1989) N: CELLULAR SUBS EITY: TO 87 MYRIS	id sequ brain:	PubMed-2 Morris C	Chordata; Rodentia;	t t t t	STANDARD;		869993221111 869963211111
SSNHLYGVAEAGAPPADPSTLYRDLPAEDSRGRQGGDAPTEDDYWG	; Score; Pred.	ω	(1989). SUBSTRATE FOR MYRISTOYLATED /		.2676596; C., Perks			PRT;	ALI	PSAC_GNEAN PSAC_GNEGN PSAC_MAIZE PSAC_SPIOLI YJ93_MYCTU YSV3_CAEEL CD3G_BOVIN ICTL_PIG HG14_HUMAN DISB_ECHCS RS16_RALSO
DPSTLYRI	No. 16;	95010788C12E2	OR PROTEIN KIN	t of	K., Brown	Craniata; Vert Sciurognathi;	update on upda rotein	85 AA	ALIGNMENTS	CYAPA CYAPA MAIZE MAIZE ORYSA SPIOL CAEEL LORYSA ECHCS ECHCS
DLPAEDSI	1; Ler 30;	268 CRC6	E-RICH C	e 80 e 87	ਸ਼ '	Vertebrata; .hi; Muridae;	e) ate) (Fragments			
GRQGGDA	Length 85;		SE C.	pro	Brooks S	• • • • • • • • • • • • • • • • • • • •	ıts).		٠	P1100000000000000000000000000000000000
\PTEDDY	22;		SUBSTRAT	⁶ ₹	•	Euteleostomi Murinae; Ra				P31173 cya O9mr11 gne P11601 zea P11794 ory P10098 spi O10865 myc O10009 cae O28074 bos P15174 hom P82466 ech Q890w0 ral
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Y9KD_STRLI
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st Local s
Atches 25
                 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation update)
01-AUG-1991 (Rel. 19, Last annotation update)
Hypothetical 9.4 kDa protein (ORF 85).
Streptomyces lividans.
Plasmid pIJ101.
Plasmid pIJ101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=88255287; PubMed=3133242;
Dublet B., Dixon E., de Miguel E., van der Rest M.;
Dublet B., Dixon E., de Miguel E., van der Rest M.;
"Bovine type XII collagen: amino acid sequence of a 10 kI
fragment from periodontal ligament reveals a high degree
fragment from periodontal ligament reveals a high degree
with the chicken alpha 1(XII) sequence.";
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NON_CONS
NON_CONS
MOD_RES
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Mammalia; Eutheria;
Bovidae; Bovinae; Bo
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                          Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales;
NCBI_TaxID=1916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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                                                                                                                                                                                                                       53 DAPTEDDYWGGYGGEDQRGEQMCPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S Lett. 233:177-180(1988).

FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
CONTAINING FIBRILS, THE COLL DOMAIN COULD BE ASSOCIATED WITH THE
SCREACE OF THE FIBRILS, AND THE COLL AND NC3 DOMAINS MAY BE
LOCALIZED IN THE PERIFIBRILLAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: PROLINES AT THE THIRD POSITION OF THE TUNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: TRIMER OF IDENTICAL CHAINS EACH CONTAINING 190 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR SIMILARITY: HIGH TO COLLAGEN ALPHA 1(IX)
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                                                                                                                                                                                                                                                                                                             Similarity
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                AA;
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                                                                                                                               STANDARD;
             Streptomycineae;
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                                                                                                                                                                                                                                                                                                                                                    8062 MW;
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29.4%;
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HYDROXYLATION.
HYDROXYLATION.
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L; Mismatches
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Pred. No. 2
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              Streptomycetaceae;
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egree of homology
                Streptomyces
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RESULT 4
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Matches 27
                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=89008081; PubMed=3170481; Kendall K.J., Cohen S.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                            Probable num process.
Bovine papillomavirus type 4.
Bovine papillomaviruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1988 (Rel. 08,
01-AUG-1988 (Rel. 08,
01-AUG-1988 (Rel. 08,
Probable E5B protein.
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Hypothetical
                                                                                                                         PIR;
                                                                                                                                                                                                          the European Bioinformatics Institute. Th
                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                              papillomavirus type 4.";
J. Gen. Virol. 68:2117-2128(1987).
                                                                                                                                                                                                                                                                                                                     MEDLINE=87282264; PubMed=3039043;
Patel K.R., Smith K.T., Campo M.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P08349;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete nucleotide sequence of the Streptomyces lividans plasmid parallol and correlation of the sequence with genetic properties.";
                                                                                              SEQUENCE
                                                                                                                                         EMBL;
                                                                                                                                                                   or send an email to license@isb-sib.ch).
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                                                                                                             Early
                                       Local Similarity hes 19; Conserv
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 2 PAAPTRPGSRARGNS-----SSNHLYGVAEAGAPPADPSTLYRDLPAEDSRGRQGGDAPT
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127129; W5WL5B
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                                                                                                             protein
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27; Conser
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Conservative
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5 AA; 9339 MW; 1
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                                                                                                11026 MW;
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31.0%;
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                                        Score 55.5; D
Pred. No. 84;
6; Mismatches
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Pred. No. 61;
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                                                                                                84978E1A86B76A9F CRC64;
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A COle S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., A Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., A Rutter S., Seeger K., Skelton S., Squares S., Squares R., A Rutter S., Seeger K., Skelton S., Squares S., Squares R., A Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
T "Deciphering the biology of Mycobacterium tuberculosis from the Transparence.";
I Nature 393:537-544(1998).
                                                                                Query Match
Best Local
                                                                  Matches
                                                                                                                       CONFLICT
                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        STRAIN-CDC 1551 / Oshkosh; Elsen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O., Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L Delicher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                CONFLICT
                                                                                                                                                                        TubercuList;
                                                                                                                                                                                     EMBL; AE007000; AAK45493.1; TIGR; MT1236; -.
                                                                                                                                                                                                               EMBL; 293777; CAB07821.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-2001 (Rel. 40, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Putative ESAT-6 like protein 4.
RV1198 OR MT1236 OR MTC1364.10.
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                              AEAGAPPADPSTLYRDLPAEDSRGRQGGDAPTEDDYWGGYGGEDQRGEQMCPGAACQ
                AQAGLLEAEHQAIIRDV---
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16; Conser
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RV1198; ...

Protein; Complete proteome.

1 -> V (IN REF. 2).

32 3 TAS -> AAG (IN REF. 2).

37 39 TAS -> AAG (IN REF. 2).

37 9928 MW; 5585B30B948BC46C CRC64;
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                                                                 Score 55; DB Pred. No. 92; 5; Mismatches
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 RESULT 6
OSTR_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996
01-OCT-1996
15-JUN-2002
                                                                                                                                                                                                                                                EMBL; L24430; AAA39855.1; -. EMBL; S67456; AAB29146.1; -. EMBL; U11541; AAB60445.1; -.
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Rahman S., Oberdorf A., Montecino
Stein G.S., Laipis P.J., Stein J.
"Muliple copies of the bone-spec:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
NCBI_TaxID=10090;
                                                                                                                                                                                          Pfam; PF00594; gla; 1
                                                                                                                                                                                                       Desbois C., Hogue D.A., Karsenty G.;
"The mouse osteocalcin gene cluster contains three genes separate spatial and temporal patterns of expression.";
J. Biol. Chem. 269:1183-1190(1994).
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                        MOD_RES
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                                                                                                       PROPEP
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                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See or send an email to license@isb-sib.ch).
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een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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BY SIMILARITY.
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(BY SIMILARITY).
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harria Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

A Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

Rutter S., Seeger K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:537-544(1998).
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STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Ewinn M.L., Haft D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg :
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                               EMBL; AF226277; AAF32406.1;
                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                       laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
-i- SIMILARITY: BELONGS TO THE ESAT6 FAMILY.
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CAB08822.1;
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RA Squices J., Baker S., Basham D., Bowman S.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA James K., Jones M., Lantin S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Holpach E.,
RA Goliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Raylor K., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Weltjens I., Vonstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Hehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT The genome sequence of Schizosaccharomyces pombe.";
RT The genome sequence of Schizosaccharomyces pombe.";
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01-FEB-1995 (Rel. 31, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
UV-induced protein uvi15.
UVI15 OR SPBC649.04.
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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Wood V., Gwilliam R.,
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Lee J.K., Kim
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     STRAIN=JY741;
MEDLINE=94324936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                       CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MT1066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=11859360;
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     PubMed=8048925,
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26.3%;
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Q -> L (IN REF. 1 AND 3; AAK48082).

S -> L (IN REF. 1 AND 3; AAK48082).

S S -> L (EN REF. 1 AND 3; AAK48082).
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Pred. No. 2.1e
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Park S.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lyne M., Lyne
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                                                                                                                                                                                                                                       MEDLINE-98295987; PubMed-9634230:
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998)."
                                             Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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16-OCT-2001 (Rel. 40, Last annot
Putative ESAT-6 like protein 6
RV2346C OR MT2411 OR MTCY98.15C.
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P95242;
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STRAIN-CDC 1551 /
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NCBI_TaxID=1773;
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                               Bishai W.;
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STRAIN-H37RV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z34300; CAA84070.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATIONARY PHASE AND IN STARVATION CONDITION. INDUCTION: BY UV LIGHT, ALKYLATING AGENTS AND HEAT SHOCK.
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genome comparison
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UV-inducible
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REQUIRED FOR THE MAINTENANCE OF VIABILITY OF CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                  Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9319 MW;
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of Mycobacterium
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Pred.
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01-JUN-1994 (Rel. 2
01-FEB-1996 (Rel. 3
Neurophysin 1 (VLDV
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01-JUN-1994
01-FEB-1996
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Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-$1115507; PubMed-2276874;
Michel G., Levy B., Chauvet M.-T., Chauvet J., Acher R.;
"Complete amino acid sequence of goose VLDV-neurophysin. Traces
"complete amino acid sequence of goose vcdv-neurophysin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Pituitary;
MEDLINE-91115507;
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P35519;
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                                                                                                                                                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                                                                                                                                             ProDom;
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HSSP; P01180; 1NPO.
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Submitted (APR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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    14
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GPRNRGRCFGPRICCGEELGCYLGTPETLRCQEESFLPTPCESGRKPCGGD-----
                                       GSRARGNSSSNHLYGVAEAGAPPADPSTL----YRDLPAEDSRGRQGGDAPTEDDYWG
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15; Conserv
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                                                                                     Conservative
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4 AA; 9954 MW; C740622D0BI
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Rel. 29, Last sequence update)
Rel. 33, Last annotation updat
(VLDV-neurophysin).
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Chordata; Craniata; Vertebrata;
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5; Mismatches
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nes 29;
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PRP5_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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Best Local :
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GRP7_DAUCA
P37704;
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MOD_RES 1
MOD_RES 8
REPEAT 15
REPEAT 36
REPEAT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Basic proline-rich proteins from human parotid saliva: covalent structures of proteins IB-1 and IB-6.";
Biochemistry 25:2387-2392(1986)
-:- DOMAIN: CONTAINS 21-RESIDUE REPEATS, TWO OF WHICH HA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAR-1987 (Rel. 04, Creat
20-MAR-1987 (Rel. 04, Last
01-OCT-1994 (Rel. 30, Last
Basic proline-rich peptide
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20-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Glycine-rich protein DC7.1 precursor.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                      "Gene expression during induction of somatic embryogenesis in carrot cell suspensions.";
Planta 183:17-24(1990).
-:- FUNCTION: MAY BE CONNECTED WITH THE INITIATION OF EMBRYOGENESIS
                                                                                                                                                                       Aleith F., Richter G.;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                          Daucus carota (Carrot)
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1994
01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                   NCBI_TaxID=4039;
                                                                                                                                                                                                                                                                                 Asteridae;
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                     OR WITH THE METABOLIC CHANGES PRODUCED BY THE REMOVAL OF AUXINS DEVELOPMENTAL STAGE: TRANSIENTLY EXPRESSED DURING EARLY
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1 PYRROLIDONE CARBOXYLIC ACID.
8 PHOSPHORYLATION.
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Pred. No. 3.5e+02;
7; Mismatches 21;
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RESULT 13
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                                                                                                                                                                                   Early protein. SEQUENCE 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Papillomavirus.
NCBI_TaxID=37111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X15706; CAA33736.1; PIR; S35715; S35715.
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                                                                                                                                                                                                           Pfam, PF02711; Pap_E4; Early protein.
                                                                                                                                                                                                                                                         EMBL; U31783; AAA79426.1; ALT_INIT. InterPro; IPR003861; Papilloma_E4.
                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus type
Viruses; dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probable E4
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nes 9; Conserv
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Last annotation update)
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Pred. No. 3.9e+02
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GLYCINE-RICH PROTEIN DC7.1.

2 APPROXIMATE REPEATS OF H-H-G(4,6)-H.
                                                                                                                 Pred. No.
                                                                                                                                       Score 48;
                                                                                                                                                                                     4FF84D4D52DBC51E CRC64;
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7C00D44637B7A364 CRC64;
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DT 01-NOV-1995 (Rel. 32,

DT 30-MAY-2000 (Rel. 39)

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InterPro: IPR003837; Glu-tRNAGIn.
Pfam; PF02686; Glu-tRNAGIn; 1.
TIGREAMS; TIGR0115; gatC; 1.
Protein blosynthesis; Ligase; Compl
SEQUENCE 96 AA; 10651 MW; 34CB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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16-OCT-2001 (Rel. 40, L
16-OCT-2001 (Rel. 40, L
Glutamyl-ENNA(Gln) amid
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Bacteria; Thermus/Deinococcus
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                                                                                                                                                                                                                                                                          NHLYGVAEAGAPPADPSTLYRDLPAEDSRGRQGGDAPTE 57
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                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                               STANDARD;
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Pred. No.
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ches 21;
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Search completed: April Job time: 19,6296 secs
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Matches 13
                                                                                                                                                                     Nitrogen fixation. SEQUENCE 71 AA;
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                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extra European Bioinformatics Institute. There are no restrict the the European Bioinformatics Institute.
                                                                                                                                                                                                    ProDom;
                                                                                                                                                                                                            Pfam; PF01106; NifU-like; 1.
                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- EUNCTION: MAY BE INVOLVED IN THE FORMATION OR REPAIR OF CLUSTERS PRESENT IN IRON-SULFUR PROTEINS (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE NIFU FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95369734; PubMed-7642138; Harriott O.T., Hosted T.J., Benson D.R.; "Sequences of nifx, nifw, nifz, nifB and nitrogen fixation gene cluster."; Gene 161:63-67(1995).
                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CpI1;
Benson D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Frankia alni.
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Frankineae; Frankiaceae; Frankia.
NCBI_TaxID=1859;
                                                                      26 EAGAPPADPSTLYRDLPAEDSRGRQGGDAPTEDDYWGGYGG 66
                                                                                                              l Similarity
13; Conserv
                                                                                                                                                                                              PD002830; N1fu; 1.
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                                                                                                            Conservative
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31.78;
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                                             -SRGRSAGSAEVHLRLTGACGC 41
                                                                                                                      Score 46;
Pred. No.
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Result
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Perfect score:
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         l number of hits satisfying chosen parameters:
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1 PPAAPTRPGSRARGNSSSNH....
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Gapop 10.0 , Gapext 0.5
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45	44	43	42	41	40	39	38	37	36	35	34	ω u	32	31	30
46	46	46	46.5	47	47	47	47	47	47.5	47.5	47.5	4.8	48	48	48.5
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nifU protein - Fra	small hypothetical		hypothetical prote	Glu-tRNA(Gln) amid	hypothetical prote	transcription fact	hypothetical prote	dynorphin precurso	RNA-binding protei	oncofetal-laminin	mucin - sheep (fra	hypothetical prote	glycine-rich prote	hypothetical prote	Ig lambda chain -

ALIGNMENTS

Query Match 12.5%; Score 59.5; DB 2; Length 74; Best Local Similarity 32.1%; Pred. No. 56;	RESULT 2 S68269 Y-box binding protein YB-1 - human (fragment) C;Species: Homo sapiens (man) C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000 C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000 C;Accession: S68269 R;Makino, Y:, Ohga, T:, Toh, S.; Koike, K.; Okumura, K.; Wada, M.; Kuwano, M.; Kohno, Nucleic Acids Res. 24, 1873-1878, 1996 A;Title: Structural and functional analysis of the human Y-box binding protein (YB-1) A;Reference number: S68269; MUID:96226173; PMID:8657568 A;Accession: S68269 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-74 <mak> A;Residues: 1-74 <mak> A;Residues: 1-74 <mak> A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1996 C;Gene: YB-1 C;Superfamily: Y box-binding protein 1; cold shock domain homology</mak></mak></mak>	Collagen alpha 1(XII) chain - bovine (fragments) C;Species: Bos prinigenius taurus (cattle) C;Dectes: Bos prinigenius taurus (cattle) C;Accession: S00802 R;Dublet, B.; Dixon, E.; de Miguel, E.; van der Rest, M. FEBS Lett. 233 177-180, 1988 A;Title: Bovine type XII collagen: amino acid sequence of a 10 kDa pepsin fragment fr A;Reference number: S00802; MUID:88255287; PMID:3133242 A;Accession: S00802 A;Molecule type: protein A;Residues: 1-15;16-48;49-86 <dubs #status="" (pro)="" 1(xii)="" 19;="" 1;="" 25;="" 29,4%;="" 3;="" 40;="" 52="" 53;="" alpha="" best="" binding;="" c;keywords:="" c;superfamily:="" cell="" chain;="" coll;="" collagen="" colled="" conservative="" extracellular="" f;6,9,12,18,24,27,30,42,51,54,65,74,77,80="" fibronectin="" gaps="" glycoprotein;="" homology;="" hydroxypro="" hydroxyproline="" iii="" indels="" local="" match="" matches="" matrix:="" mismatches="" modified="" no.="" pred.="" query="" repeat="" similarity="" site:="" td="" type="" von="" <=""><td>RESULT 1 S00802</td></dubs>	RESULT 1 S00802

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Вb
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thors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.; Lie: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Reference number: A70500; MUID:98295987; PMID:9634230

A; Accession: B70809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70809
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hypothetical 10.8K proto; Species: Streptomyces
                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AL022004; GB:AL123456; NID:g3261550; A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-60 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вb
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A; Residues: 1-97 <SEE>
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                                       A30924
                                                                                                                                                                                                                                                                                                        A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AL096884; PIDN:CAB51462.1; GSPDB:GN00070; SC0EDB:SC4G6.39c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein Rv0810c - Mycobacterium tuberculosis (strain H37RV)
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cession: T35099
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                                                                                                                   RGRAKAKQTKVARELKYSSPQTDFQRLQRELSGTGT-DRLDGDGPSDDDSW 52
                                                                                                                                                       RARGNSSSNHLYGVAEAGAPPADPSTLYRDLPAEDSRGRQGGDAPTEDDYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PADPSTLYRDLPAEDSRGRQGGDAPTEDDYWGGYGGEDQRGEQMCPGAA 79
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                 10.8K protein
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                   85) -
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                                                                                                                                                                                                            Score 56.5;
Pred. No. 8
                                                                                                                                                                                            Mismatches
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                   Streptomyces lividans
                                                                                                                                                                                                                ; 88
                                                                                                                                                                                                                                DB
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                                                                                                                                                                                                                                Length
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                   plasmid
                                                                                                                                                                                                                                                                                                                              PIDN:CAA17616.1; PID:e125395
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                   р1J101
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A; Authors: Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
                                                                                                                                                                                                                                                                                hypothetical protein Rv1198 - Mycobacterium tuberculosis (strain H37RV) c;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999 C;Accession: D70608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Patel, K.R.; Smith, K.T.; Campo, M.S.
J. Gen. Virol. 68, 2117-2128, 1987
A;Title: The nucleotide sequence and genome organization A;Reference number: A92795; MUID:87282264; PMID:3039043 A;Accession: I27129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete nucleotide sequence of the Streptomyces A;Reference number: A91888; MUID:89008081; PMID:3170481 A;Accession: A30924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-95 <PAT>
C;Superfamily: bovine papillomavirus type 4 E5B protein
C;Keywords: early protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESB protein - bovine papillomavirus type 4
C;Species: bovine papillomavirus type 4
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 24-Feb-1994
C;Accession: I27129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
C;Accession: A30924
A;Cross-references: GB:Z93777; GB:AL123456; A;Experimental source: strain H37Rv
                                          A; Residues: 1-94 <COL>
                                                            A; Molecule type: DNA
                                                                                     A; Status: preliminary;
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A; Residues: 1-85 <KEN>
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J. Bacteriol. 17
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Best Local
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nes 19; Conserv
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27; Conserv
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                                                                                       nucleic acid sequence not shown; translation not
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Pred. No. 1.2e-
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55.5; DB 1;
Pred. No. 1.7e+02;
6; Mismatches 31;
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1.2e+02;
                      NID:g3261726;
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                           PIDN:CAB07821.1; PID:e31107
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osteocalcin-related protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
C:Accession: 161188; 149073
R:Desbois, C:; Hogue, D.A.; Karsenty, G.
J. Biol. Chem. 269, 1183-1190, 1994
A:Title: The mouse osteocalcin gene cluster contains three genes
                                                                                                                                          RESULT 10
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C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
C;Accession: I67413
R;Rahman, S.; Oberdorf, A.; Montecino, M.; Tanhauser, S.M.; Lian, J.B.; Steindocrinology 133, 3050-3053, 1993
A;Title: Multiple copies of the bone-specific osteocalcin gene in mouse and A;Accession: I67413
A;Accession: I67413
                                                                                                                                                                                                                                                                                                           C; Superfamily:
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C;Species: Notophthalmus viridescens, Triturus viridescens (east
C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
C;Accession: S55780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-89 <SAV>
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Best Local
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A;Gene: Rv1198
                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; translated from GB/EMBL/DDBJ lecule type: DNA sidues: 1-95 <RES>
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Hie: Differential regulation of Hox C6
Liference number: $55780; MUID:95311312;
Rocession: $5578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: mRNA
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Best Local
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                                                                                                                                                                                         3 AAPTRPG-----SRARGNSSSNHLYGVAEAGAPPADPSTLYRDL----PAEDSRGROGG
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20; Conserv
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11; Conservative
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16; Conservative
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Pred. No. 2.9e+02;
2; Mismatches 28;
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Pred. No. 2.
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Pred. No.
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2.7e+02;
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hange 07-May-1999
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                                                              20-Aug-1999
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A; Molecule type: DNA
A; Residues: 1-96 <KIN>
A; Cross-references: GB;
C; Superfamily: unassign
                                                                                                                                                                                                                      C.Accession: 844982
R.Kingston, I.B.; Wainwright, S.M.; Cooper, R.Kingston, Parasitol. 37, 137-146, 1989
                                                                                                                       A; Status: preliminary
                                                                                                                                          MOl. Biochem. Parasitol. 37, 137-146, 1989
A;Title: Comparison of collagen gene sequences in Ascaris
A;Reference number: A44982; MUID:90136710; PMID:2482444
A;Accession: B44982
                                                                                                                                                                                                                                                                                                                    collagen COLA4 - pig roundworm
C;Species: Ascaris suum (pig roundworm)
C;Date: 14-May-1993 #sequence_revision
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B44982
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C. Species: Synechocystis sp.
A; Variety: PCC 6803
C. Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C; Accession: S77116
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Po, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamadu, T.; Yamadu, T.; Watanabe, A.; Yamadu, T.; Watanabe, A.; Yamadu, T.; Watanabe, A.; Yamadu, T.; Y
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A; Residues: 1-90 <KAN>
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A; Residues: 1-95 <RE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
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A:Molecule type: DNA
A:Residues: 1-95 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 ATETGPESDKAFMSKQEGNKVVNRLRRYLGASVESPDPLEPTRELCELDFACDELSNQYG
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nces: GB:J04655; NID:g159654; PIDN:AAA29370.1; unassigned collagens
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33.3%;
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Pred. No. 3e+02;
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Pred. No. 2.9e+02;
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Watanabe, A.; Yamada,
                  PID:g159655
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Yamada, M.; Yas
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Best Local Similarity
The hes 23; Conserve
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A; Pritle: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixin A; Reference number: A95842; MUID:21396508; PMID:11481431
A; Accession: B95850
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B95850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymEc; Species; Sinorhizobium meliloti (c.pate: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 cession: B95850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A96039; MUID:21368234; PMID:11474104
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A; Residues: 1-61 <KUR>
                                                                                                                                                                                                                 hypothetical protein C37A5.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tc;Accession: T19805 R;White, S.
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T19805
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-89 <WIL>
A;Cross-references: EMBL:292828; PIDN:CAB07335.1; GSPDB:GN00019; CESP:C37A5.8
A;Experimental source: clone C37A5
C;Genetics:
C;Genetics: CESP:C37A5.8
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                                                                                                                                                    submitted to the EMBL Data Library, A; Reference number: Z19180 A; Accession: T19805
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18; Conserv
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Pred. No. 4e+02;
5; Mismatches 36;
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pred. No. 2.8e+02;
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hypothetical protein Rv3619c, Rv1037c - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999 C;Accession: D70560; H70624 C;Accession: H70624 C;Accession: D70560; H70624 C;Access
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A; Introns: 52/2
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A;Experimental source: strain H37RV
C;Genetics:
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A; Residues: 1-94 <COL>
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ALIGNMENTS

RESULT 1
ABG08602
ID ABG0 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations ${\bf r}$ 31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167. WPI; 2001-639362/73. N-PSDB; AAS72789. Drmanac RT, Liu C, 30-MAR-2001; 2001WO-US08631. 11-OCT-2001. Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder. ABG08602 standard; Protein; 88 (HYSE-) HYSEQ WO200175067-A2 Homo sapiens. Novel human diagnostic protein #8593. 13-FEB-2002 (first entry) ABG08602; INC. Tang ŢΥ A A

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CC Specification, but was obtained in electronic format directly from WIPO at figure as a sequences.
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tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorders; arthitis; inflammation.
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WPI; 2001-514838/56
                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                       28-FEB-2000;
18-MAY-2000;
                                                                                                                                                                                                                                                                                26-FEB-2001; 2001WO-US04927
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                                                           YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYK - - PPGGGRGTQEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAAPTRGPGARVRGHPPPGAPPIRKAATAPKLGCGVGGAPSPKQTMREKALHVAPATPRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system disorders;
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                                                           Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 AA;
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                                                                                                                                                                                       2000US-0515126
2000US-0577409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell proliferation; cell differentiation; gene therapy;
                                                                 Drmanac
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RESULT 3
AAU22202
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Matches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
                                                                                                                                                                                                                                      ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; bacterial infection; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; tissue regeneration; anti-infertility.
                                                                                                                                                                                                                                                                                                                                                      chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAI90699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 24660; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                             Cardiovascular system antigen; human; mouse; rabbit; goat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU22202 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                        17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cardiovascular system antigen polypeptide SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation.
                                                                                                                                                                        WO200155321-A2
                                                                                                                                                                                                          Homo sapiens
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les 22; Conserv
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nilarity 32.4%;
Conservative
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2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
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                                                                                                        2001WO-US01340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
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Pred. No. 4
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11-SEP-2000
22-AUG-2000
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23-AUG-2000
23-AUG-2000
23-AUG-2000
23-AUG-2000
23-AUG-2000
21-SEP-2000
01-SEP-2000
01-SEP
               2000US-0190076.
2000US-0190176.
2000US-0205451.
2000US-02154186.
2000US-0216647.
2000US-0216647.
2000US-0216647.
2000US-0217496.
2000US-0217496.
2000US-0217496.
2000US-0217496.
2000US-02254518.
2000US-022526.
2000US-023124.
2000US-
          13-OCT-2000

20-OCT-2000

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20-OCT-2000

20-OCT-2000

08-NOV-2000

17-NOV-2000

17-NO
                                                                         New cardiovascular system related polynucleotides and polypeptides useful for diagnosing, treating and/or preventing disorders of the cardiovascular system -
  Sequences AAU21852-AAU22466 represent the
                                               Claim 11;
                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                    Rosen
                                                                                                                                                                                                                                                                        (HUMA-) HUMAN
                                                                                                                                                                     2001-451930/48
)B; AAS35476.
                                                                                                                                                                                                                                 CA,
                                               SEQ
                                                                                                                                                                                                                               Barash SC,
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2000US-0241960
2000US-0241785
2000US-0241786
2000US-0241808
2000US-0241808
2000US-0241809
2000US-0246474
2000US-0246477
2000US-0246477
2000US-0246477
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2000US-0249214
2000US-0249215
2000US-0249216
2000US-0251938
2000US-0251868
2000US-0251868
2000US-0251989
2000US-0251989
                                               ID No
                                                                                                                                                                                                                                                                           GENOME
                                             976;
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                                                                                                                                                                                                                                 Ruben
                                                                                                                                                                                                                                                                           INC
                                           674pp;
                                                                                                                                                                                                                                 SM;
                                           English.
cardiovascular system antigen
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RESULT 4
ABB17420
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31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                        Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chemotaxis. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human nervous system related polypeptide SEQ ID NO 6077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB17420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB17420 standard; Protein;
                                                                                                                                                                                                                                                                   WO200159063-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JAN-2002
                                                                                                                                                                                                       17-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGTPPTRPGSPRGGGGEPIFWGKKRGKGGNPPPGPKTPPK-XPKXFGKGERGG----EF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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 2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
2000US-0198123.
2000US-0198123.
2000US-0205515.
2000US-020467.
2000US-0214886.
2000US-0215135.
2000US-0215135.
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                                                                                                                                                                                                       2001WO-US01334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.4%;
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Pred. No. 5.3;
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            07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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22-AUG-2000
23-AUG-2000
30-AUG-2000
01-SEP-2000
01-SEP-2000
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05-SEP-2000
06-SEP-2000
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14-AUG-2000
18-AUG-2000
22-AUG-2000
                      14-SEP-2000

21-SEP-2000

21-SEP-2000

25-SEP-2000

25-SEP-2000

26-SEP-2000

27-SEP-2000

27-SEP-2000

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21-SEP-2000

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21-OCT-2000

21-OCT-2000
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14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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2000US-0225758
2000US-0225759
2000US-0226279
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2000US-0225270.
2000US-0225447.
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2000US-0224518.
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2000US-0226868.
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2000US-0227009.
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2000US-0232401
2000US-0233063
2000US-0233063
2000US-0233065
2000US-0234223
2000US-0234223
2000US-0234274
2000US-0234997
2000US-023498
2000US-0235834
                                        2000US-0237038.
2000US-0237039.
2000US-0237040.
2000US-0239935.
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2000US-0249960.
2000US-0241785.
2000US-0241786.
2000US-0241787.
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2000US-0236327.
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08-NOV-2000;
17-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
                                       The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
                                                                                                   Claim 11;
                                                                                                                                             Nucleic
                                                                                                                                                                                                                                                                                                                               05-DEC-2000;
05-DEC-2000;
                                                                                                                                   useful for
                                                                                                                                                                                                                     ( HUMA - )
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                                                                                                                                                                2001-541565/60.
DB; ABA13746.
                                                                                                                            acids encoding 3224 human nervous system antigen polypeptides, for preventing, diagnosing and/or treating nervous system
                                                                                                                                                                                                                    HUMAN GENOME
                                                                                                  SEQ
                                                                                                                      preventing,
i metastases
                                                                                                                                                                                                Barash
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2000US-0249309
2000US-0249300
2000US-0251391
2000US-0251391
2000US-0251160
2000US-0251986
2000US-0251479
2000US-0251856
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Best Local
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                                                                                                                  Propionibacterium acnes
                                                                                                                                                                                                             Skeiky YAW,
                                                                                                                                                                                                                                                         21 APR-2000; 2000US-199047P
02-JUN-2000; 2000US-208841P
07-JUL-2000; 2000US-216747P
                                                                                                                                                                                               L'maisonneuve
                                                                                                                                                                                                                                                                                                                                                                                                           SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAPHO syndrome; synovitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                               WO200181581-A2.
                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes immunogenic protein #23762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU62866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                       2001-616774/71.
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20; Conser
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                                                                                                          acne vulgaris
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                                                                                                                                                                                          Υ,
                                                                                                                  polypeptides and nucleic acids useful for diagnosing infections, especially useful
                                                                                                                                                                                          Mitcham JL, Wang SS, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
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                                                                                                                               for
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pustulosis, P. acnes is

hypertosis and also involved

involved in

osteomyelitis), uveitis in infections of bone, jo

joints

and endophthalmitis

immunogenic are used in

Example 1;

SEQ ID

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24061; 1069pp;

English.

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogen polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

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RESULT 6
ABP35282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used therefore treat p. acnes infections. The antibodies may also be used diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the prin specification, but was obtained in electronic format directly from WI specification, but was obtained in electronic format directly from WI specification, but was obtained in electronic format directly from WI specification, but was obtained in electronic format directly from WI specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; behaviour; cancer; proliferative disorder; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; cardiant; hypotensive; antithyroid; antiinflammator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dermatological; analgesic; virucide; antibacterial; fungicide
Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                                       N-PSDB; ABN79308
                                                                                                                                                                                         (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                        24-MAY-2000; 2000US-206690P
                                                                                                                                                                                                                                                                                       24-MAY-2001; 2001WO-US17076
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                WPI; 2002-106200/14.
                                                                                                                                                 Leach MD
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Pred. No. 11;
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conjugations at least 80% identical to the ORFI-ORF4334 (collectively correferred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFI-ORF4334 (collectively correferred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX correction for ORFX proteins, methods of detecting ORFX proteins, antibodies goolynucleotides, methods of screening for modulators of ORFX proteins, and methods of screening individuals for a predisposition or activity, and methods of screening individuals for a predisposition to an activity, and methods of screening individuals for a predisposition, and corrected disorder. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, haematopoiesis regulation, cell differentiation, haemostatic activity, thrombolytic activity, chemotactic/correceptor/ligand, antiinflammatory activity, thrombolytic activity, and may also be involved in the determination of boddily characteristics, fertility and behaviour. ORFX proteins, currently activity and behaviour of the determination of concers, colleged and antibodies may be used in the treatment of cancers, colleged and antipodies and benign tumours.
                                                        neurological disorders such as epilepsy and Alzheimer's disease, concerning the disorders such as epilepsy and Alzheimer's disorders related to cardiovascular diseases, immune system disorders, disorders related to corgan transplantation, disorders of tissue growth and regeneration, concerning diseases, and infectious diseases caused by viral, bacterial, congress expenses, and infectious diseases caused by viral, bacterial, congress and other pathogens. ORFX nucleic acids may also be used as a congress of primers and probes, in the detection of ORFX genomic sequences congress, in genetic diagnosis, and in forensic biology. The ORFX concerning in genetic diagnosis, and in forensic biology. The ORFX concerning and additionally be used to produce transgenic animals concerning and additionally be used to produce transgenic animals concerning and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the concerning concerning the ORFX associated diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      designated ORF (open reading frame) 1-4534, and sequence ABN79587 represent cDNAs encoding them. The invention al polypeptides at least 80% identical to the ORF1-ORF4534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hyperproliferative disorders and disorders related to organ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB31028-ABB35561 represent 4534 novel human proteins d ORF (open reading frame) 1-4534, and sequences ABM/5054-represent cDNAs encoding them. The invention also encompasses
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Вр QY Query Match Best Local Matches 40 DLPAEDSRGRQG----GDAPTEDDYWGGYG----GEDQRGEQMCPGAACQAP 3 DLPLSQESGGQWPSLGDGPSA-LIWGGFGLQVSGEQLRSYLQRPGASRLAP 20; Similarity Conservative 13.7%; 39.2%; ω,. Score 65; DB Pred. No. 8.9; Mismatches 23; 20; Length 56 52 8 Gaps

ω

Sequence

56

AA;

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RESULT 7
AAB873
IID AAB88
IID AAB88
AC AAB86
XX AAB6
XX AAB6
XX AAB6
XX Huma
DE Huma
XX Huma
KW foet
KW foet
KW infin
KW infin
KW Parl
KW Parl
KW Gary
KW gass
KW gass
KW endd
KW eend
KW eend
XX
                                                                                                                                                                                                        AAB87388 standard;
                                                                                                                                                              22-MAY-2001 (first entry)
                                                                                                                                                                                   AAB87388;
                                                                                                                                           encoded secreted protein HFXDK20,
                                                                                                                                                                                                          Protein; 94
                                                                                                                                                                                                            AA
                                                                                                                                              SEQ ID NO:129
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Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; inflammation; allergy; neurological disorder; Alzheimer's disease; cell endocrine disorder; infection; wound heacell culture; chemotaxis; food additive; Human gastrointestinal disorder; gene pregnancy-related disorder; on; wound healing; vulnerary

Homo sapiens

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RESULT 8
ABG65366
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                                                                                                                                                     В
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                                                                                                                                                                                                                                                                                                                             ARF91858-AAF91929 represent cDNAs corresponding to 52 human secreted CC AAB87414-AAB87342-AAB87341 represent the proteins they encode. AAB87414-AAB87454 represent human secreted protein fragments. The genes CC and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene CC therapy. Pathological conditions can be diagnosed by determining the CC amount of the new protein in a sample or by determining the presence of CC 2 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of CC proliferative disorders, cancer, tumours, foetal and developmental CC allergies, neurological disorders (e.g., Alzheimer's diseases, CC allergies, and infections. The proteins can also be used to aid wound the pathelial cell proliferation, to prevent skin aging due to gustrointestinal disorders, pregnancy-related disorders, endocrine thealing and epithelial cell proliferation, to prevent skin aging due to constact ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

CC allergiating symptoms associated with the disorders mentioned above, and confidency (CC indunosorbent assay (ELISA). The present sequence represents a human cCC indunosorbent assay (ELISA). The present sequence represents a human cCC indunosorbent assay (ELISA). The present sequence represents a human cCC indunosorbent assay (ELISA). The present sequence represents a human cCC indunosorbent assay (ELISA).
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Matches
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                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 559; 607pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-203081/20.
N-PSDB; AAF91904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ni J, Baker KP, Birse CE, Fiscella M, Soppet DR, Young PE, Ebner R, Duan DR, Moore PA, Shi Y, Wel Y, Florence KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-SEP-1999;
03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-AUG-2000; 2000WO-US24008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2001
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                                                                          83
                                                                                                               73
                                                                                                                                                     37
                                                                                                                                                                                 24 VAEAGAPPA----DPSTLYRDLPAEDSRGRQGGDAPTEDD-----YWGGYGGEDQRGE 72
                                                                                                                                                                                                                                                    Local Similarity
                                                                                                             QMCPGAACQAPP
                                                                                                                                             VSTSPPPPATRCPDESELYRD-----PGEAPLEADQAERGAAHEGGHPGRD----
                                                                          ---PWGARRGPP
                                                                                                                                                                                                                                                                                                           94 AA;
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0152315.
99US-0152317.
                                                                          91
                                                                                                                                                                                                                                                13.78;
                                                                                                                                                                                                                          Score 65; DB:
Pred. No. 16;
6; Mismatches
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Olsen HS,
                                                                                                                                                                                                                                                                22;
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                                                                                                                                                                                                                                                                Length 94
                                                                                                                                                                                                                          Indels
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eur DW;
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                                                                                                                                                                                                                        Gaps
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Qy
                                 В
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                                                                                                                      Query Match
                                                                                            Matches
                                                                                                                                                                            diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcrative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoletic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-APR-2000;
25-APR-2000;
21-DEC-2000;
                                                                                                                                                                                                                                                                                                The present invention relates to albumin fusion proteins comprising a therapeutic protein x and human albumin (HA, also known as human seru albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer;
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 1949-1950; 2102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-010886/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuroprotective; antiparkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Albumin fusion protein; therapeutic protein X;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
   73
                                 37 VSTSPPPPATRCPDESELYRD
                                                       24 VAEAGAPPA----DPSTLYRDLPAEDSRGRQGGDAPTEDD-----YWGGYGGEDQKGE 72
                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion protein for treating disease e.g. diabetes comprises {\tt umin} fused to a therapeutic protein -
 QMCPGAACQAPP 84
                                                                                          l Similarity
23; Conserv
                                                                                                                                                     94
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                                                                                          Conservative
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2000US-199384P.
2000US-256931P.
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                                                                                                                                                     AA:
                                                                                                      13.7%;
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                                                                                         6,
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                                                                                                         Pred.
                                                                                                                      Score 65;
                              ----PGEAPLEADQAERGAAHEGGHPGRD----
                                                                                       Mismatches
                                                                                                       No. 16;
                                                                                                                      DB
                                                                                                                      23;
                                                                                         15;
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                                                                                                                  Length 94;
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorder;
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                                                                                    Gaps
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RESULT 9 AAG26174

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25-FEB-1999

05-MAR-1999

23-MAR-1999

23-MAR-1999

23-MAR-1999

21-APR-1999

01-APR-1999

01-APR-1999

01-APR-1999

08-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

24-MAY-1999

05-MAY-1999

07-MAY-1999

14-MAY-1999

14-JUN-1999

16-JUN-1999

17-JUN-1999

18-JUN-1999

18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence; corn.
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 990S-0121825
990S-012548
990S-0125788
990S-0125788
990S-012678
990S-012678
990S-0136714
990S-0130871
990S-0130871
990S-0130871
990S-0132484
990S-0132485
990S-0132485
990S-0134218
990S-0135224
990S-0135224
990S-0136221
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       18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
11-JUN-1999;
21-JUN-1999;
22-JUN-1999;
23-JUN-1999;
23-JUN-1999;
24-JUN-1999;
20-JUN-1999;
21-JUN-1999;
21-JU
       990S-0139461

990S-0139463

990S-0139750

990S-0139873

990S-0140893

990S-0140893

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990S-0141842

990S-0142803

990S-0142803

990S-0142803

990S-0142972

990S-0144381

990S-0144331

990S-0144331

990S-0144332

990S-0144333

990S-0145918

990S-0147303

990S-0147935

990S-0149368

990S-0149368

990S-0149329

990S-0149329

990S-0149929
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RESULT 10
AAU22312
        DX DX EX E
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Best Local Similarity 33.9
Matches 20; Conservative
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25-AUG-1999

26-AUG-1999

27-AUG-1999

27-AUG-1999

30-AUG-1999

31-AUG-1999

31-SEP-1999

11-SEP-1999

15-SEP-1999

15-SEP-1999

22-SEP-1999

23-SEP-1999

24-SEP-1999

24-SEP-1999

25-OCT-1999

06-OCT-1999

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08-OCT-1999

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26-OCT 1999
26-OCT 1999
26-OCT 1999
26-OCT 1999
26-OCT 1999
27-OCT 1999
28-OCT 1999
28-OCT 1999
29-OCT 1999
   Human cardiovascular system antigen polypeptide
                                        17-DEC-2001
                                                                          AAU22312;
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                                                                                                                                                                                                            PPAAPTRPGSRARGNSSSNHLYGVAEAGAPPADPSTLYRDLPAEDSRGRQGGDAPTEDD 59
                                                                                                                                                                                     PPPPPTR---RLKSLPASCHL--ASAPGSPPATQTSSVRS--PRDRTGDHGGPAHRRPD
                                                                                                         standard; Protein; 68 AA
                                     (first entry)
                                                                                                                                                                                                                                                                                                                            99US-0151080
99US-0151338
99US-0151338
99US-0151337
99US-015263
99US-0153070
99US-0153070
99US-0154078
99US-015559
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99US-0157117
99US-0157765
99US-0158022
99US-0158022
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99US-0158023
99US-0158037
99US-0159331
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99US-01614064
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                                                                                                                                                                                                                                                                        13.6%;
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Pred. No. 18;
6; Mismatches
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                                                                                                                                                                                                                                                            26;
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     SEQ
                                                                                                                                                                                                                                                                                          Length
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     IJ
     NO.
                                                                                                                                                                                                                                                                                              96;
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                                                                                                                                                                                                                                                          Gaps
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     31-JAN-2000
04-FEB 2000
24-FEB 2000
16-MAR 2000
17-MAR 2000
17-MAR 2000
19-MAR 2000
19-MAR 2000
11-JUN-2000
10-JUN-2000
11-JUL-2000
11-AUG-2000
11-AUG
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2000US-0229509.
2000US-0229513.
2000US-0230437.
2000US-0231242.
2000US-0231244.
2000US-0231244.
2000US-0231244.
2000US-0231244.
2000US-0231244.
2000US-0231244.
2000US-0231266.
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2000US - 0227182
2000US - 0227109
2000US - 0228924
2000US - 0228924
2000US - 02293487
2000US - 0229344
2000US - 0229344
2000US - 0229344
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2000US-0225214

2000US-0225267

2000US-0225267

2000US-0225268

2000US-0225270

2000US-0225447

2000US-0225757

2000US-0225759

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2000US-0216880.

2000US-0217487.

2000US-0217496.

2000US-0218290.

2000US-0218290.

2000US-022964.

2000US-0224518.

2000US-0224519.
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2000US-0186350.
2000US-0189974.
2000US-0190076.
2000US-0199123.
2000US-0205515.
2000US-0209467.
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2000US-0215135.
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Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog; antirhemmatlo; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; beast; liver; cardiovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection, ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; tissue regeneration; anti-infertility.

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25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
20-CCT-2000;
02-CCT-2000;
03-NOV-2000;
04-NOV-2000;
08-NOV-2000;
08-NO
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14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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17-NOV-2000;
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21-SEP-2000;
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2000US-0232398.
2000US-0232399.
2000US-0232401.
2000US-0232401.
2000US-0233063.
                                                 2000US-0246524

2000US-0246525

2000US-0246526

2000US-0246527

2000US-0246610

2000US-0246610

2000US-0246611

2000US-0246611

2000US-0246611

2000US-0249201

2000US-0249201

2000US-0249210

2000US-0249210

2000US-0249211

2000US-0249211

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2000US-0249246

2000US-0249265

2000US-0249297

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2000US-0246476.
2000US-0246477.
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2000US-0236327
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2000US-0233065
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2000US-0235834.
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2000US-0234274.
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2000US-0244617.
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2000US-0246523.
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Qy
                                                                                                                                                                                                         CC prevention of various types of disorders in e.g. humans, mice, rabbits, CC goats, horses, cats, dogs, chickens or sheep. A pathological condition CC can be determined by detecting the presence or absence of a mutation in a CC cardiovascular system antigen polynucleotide. The treatable disorders CC include autoimmune diseases such as rheumatoid arthritis, CC hyperproliferative disorders such as rheumatoid arthritis. CC cardiovascular disorders such as cardiac arrest, cerebrovascular CC disorders such as cardiac arrest, cerebrovascular CC disorders such as cerebral ischaemia, nervous system disorders such as a Zardiac arrest, viruses and fungi, CC cardiac disorders such as corneal infection, endocrine disorders such as CC crohn's disease, infections caused by bacteria, viruses and fungi, CC crohn's disease, renal disorders such as glomerulonephritis and cCC crohn's disease, renal disorders such as glomerulonephritis and CC crohn's disease, renal disorders such as glomerulonephritis and cCC crohn's disease, renal disorders such as glomerulonephritis and cCC crohn's disorders such as asthma and pleurisy. The polypeptides can can be used to aid wound healing, to prevent skin aging due to sunburn, CC to maintain organs before transplantation, to regenerate tissues and in
                                              Query Match
Best Local S
Matches 19
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05-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cardiovascular system related polynucleotides and polypeptides useful for diagnosing, treating and/or preventing disorders of the cardiovascular system .
                                                                                                                                               Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides of the invention. Cardiovascular system antigens and the associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits
                                                                                                                                                                                                chemotaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences AAU21852-AAU22466 represent the cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigens and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID No 1086; 674pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME
                                              y Match 13.5%;
Local Similarity 35.2%;
hes 19; Conservative
      30
                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
  PPADPSTLYRDLPAEDSRGRQGGDAPTEDDYWGGYGGEDQRGEQMCPGAACQAP
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2000US-0251988.
2000US-0256719.
2000US-0251479.
2000US-0251856.
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2000US-0254097.
2001US-0259678.
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2000US-0251869.
2000US-0251989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCI INC
                                              ; Score 64; DB;
; Pred. No. 14;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM;
                                                                                          22;
                                                     18;
                                                                                        Length 68;
                                                     Indels
                                                                                                                                                        part of the printed directly from WIPO
                                                     16;
           83
                                                     Gaps
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AAM84780
IID AAM8
XX
AC AAM8
AC AAM8
DT 07-N
XX
DE Huma
XX
KW Huma
KW Cytc
XX
PN WO2(
                                                                                                                                                                                                                                                                 Вb
                                                         cytostatic; gene therapy; vaccine; metastasis
                                                                       Human; immune; haematopoietic; immune/haematopoietic antigen; cancer:
                                                                                                   Human immune/haematopoietic antigen SEQ ID NO:12373
                                                                                                                                                                                        AAM84780 standard; Protein; 85
                                                                                                                                                                                                                                                                 PPVSPP--HEDLPA-----DKQQEGTCCEGY----RNVGSCPGAPCQGP
                                                                                                                                 (first entry)
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WO200157182-A2

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31-JAN-2000

24-FEB-2000

24-FEB-2000

16-ARR-2000

17-MAR-2000

19-MAY-2000

19-MAY-2000

19-MAY-2000

21-JUL-2000

11-JUL-2000

11-JUL-2000

11-JUL-2000

11-JUL-2000

14-AUG-2000

14-SEP-2000

25-SEP-2000

21-SEP-2000

21-SEP-2000
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        2000US-0179065.
2000US-01186350.
2000US-01186350.
2000US-01186350.
2000US-0119874.
2000US-0119877.
2000US-0216880.
2000US-0216880.
2000US-0218290.
2000US-0218290.
2000US-0224518.
2000US-0224518.
2000US-0225213.
2000US-0225213.
2000US-0225213.
2000US-0225214.
2000US-0225214.
2000US-0225216.
2000US-0225216.
2000US-0225217.
2000US-0225217.
2000US-0225218.
2000US-022528.
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2000US-022934.
2000US-023124.
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29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
22-CCT-2000
02-CCT-2000
03-CCT-2000
04-NOV-2000
08-NOV-2000
09-DEC-2000
08-DEC-2000
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           Rosen
                                   ( HUMA - )
          CA,
                                   HUMAN
        Barash
                                                         2000US-0235367
2000US-0235368
2000US-0235369
2000US-0235802
2000US-0237039
2000US-0237039
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2000US-0239937
2000US-0241787
2000US-0241787
2000US-0241808
2000US-0241808
2000US-0241826
2000US-0246478
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2000US-0246511
2000US-0249211
2000US-0249218
2000US-02511868
2000US-02511868
2000US-0251189
2000US-0254997
                                  GENOME
        sc,
                                   SCI
       Ruben
       SM;
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SSSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cc amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cc artivity, and can be used in gene therapy and vaccine production. (I) cc artivity, and can be used in gene therapy and vaccine production. (I) cc proteins and polynucleotides may be used in the prevention, diagnosis and cc example, they may be used to treat disorders associated with inappropriate (I) expression. For cc expression by rectifying mutations or deletions in a patient's genome cc expression by rectifying mutations or deletions in a patient's genome cc that affect the activity of (I) by expressing inactive proteins or to complement the patients own production of (I). Additionally, (I) cc supplement the patients own production of (I). Additionally, (I) protein. (I) proteins and polynucleotides may be used to prevent, the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, cancers and cancer metastases of haematopoietic related diseases, especially concers and cancer metastases of haematopoietic antigen genomic concers and cancer metastases of haematopoietic antigen genomic represent human immune/haematopoietic antigen genomic represent sequences used in the exemplification of the present invention. AAK54942 to AAK54950 and AAM82169
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Best Local
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N-PSDB; AAK57561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; SEQ ID NO 12373; 3071pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                            SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU57626 standard; Protein; 51
                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes immunogenic protein #18522
                                                                                      21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                      01-NOV-2001.
                                                                                                                                                                                                                                                                            Propionibacterium
                                                                                                                                                                  20-APR-2001; 2001WO-US12865
L'maisonneuve
                 Skeiky YAW,
                                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 T 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 T 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PPAAPTRPGSRARGNSSSNHLYGVAEAGAPPADPSTLYRDLPAEDSRGRQGGD-----AP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 PPRA-TLPGAGLRG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
   Persing DH,
s J, Zhang Y,
                                                                                                                                                                                                                                                                                    acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.1%;
37.7%;
                     Mitcham JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----AGLEGAGRSALRRRGPASDEGGREGTPVAGHCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 62;
Pred. No.
     Jen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
       ß
       Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
30;
                         Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Length 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                         SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                             Bhatia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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CC presence of absence of P. acnes in a patient comprises contacting the correct with a binding agent that binds to the proteins and conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelltis), uvestis and endophthalmitis. Cc pustulosis, hypertosis and osteomyelltis) uvestis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central P. acnes is also involved in infections of bone, joints and the central Cc presence or absence of p. acnes in a patient comprises contacting the Cc presence or absence of p. acnes in a patient comprises contacting a cc presence or absence of p. acnes in a patient comprises contacting a cc presence or absence of p. acnes in that binds to the proteins of the invention cc and determining the amount of bound protein in the sample. The CC and determining the amount of bound protein in the sample of the compression and activity of P. acnes plypeptides and compression and activity of P. acnes plypeptides and cc downregulate expression and activity of P. acnes plypeptides and cc diagnostic agents for determining P. acnes presence, for example, by cc diagnostic agents for determining P. acnes presence, for example, by cc enzyme linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed cc at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
AAU50651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
В
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID No 18821; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences AAU39105-AAU68017 represent Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                               21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                      SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitls; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                             AAU50651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU50651 standard; Protein;
                                                                                                                                                                               01-NOV-2001
                                                                                                                                                                                                              WO200181581-A2
                                                                                                                                                                                                                                                                             dermatological;
                                                                                                                                                                                                                                            Propionibacterium
L'maisonneuve
               Skeiky YAW,
                                              (CORI-) CORIXA CORP
                                                                                                                                                20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 RPGSRARGNSSSNHLYGVAEAGAPPADPSTLYRDLPAEDSRGROGGDAPTEDD-YWG 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                               ; 2000US-199047P.
; 2000US-208841P.
; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
 Persing DH, rang Y,
                                                                                                                                                                                                                                                                                osteopathic; neuroprotectant
                                                                                                                                                                                                                                                   acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.8%;
     Mitcham JL,
, Jen S, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 61;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                  protein #11547
        Carter D;
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22;
                      Wang SS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                           P
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are used in
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RESULT 14
AAO08818
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic CC polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosts of medical conditions caused by Particularian and endephasis of medical conditions caused by Particularian and Endemyelitis), uveitis and endephthalmitis. Acne, CC pustilosis, hypertosis and osteomyelitis), uveitis and endephthalmitis. CC enervous system, however it is particularly involved in the inflammatory presence or absence of P. acnes in a patient comprises contacting the gresence or absence of P. acnes in a patient comprises contacting a and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies CC specific for P. acnes proteins. These antibodies can be used to therefore treat P. acnes infections. The antibodies can be used to CC clasgostic agents for determining P. acnes presence, for example, by CC enzyme linked immunosorbent assay (BIISA).

CC specification, but was obtained in electronic format directly from WIPO XXX
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                   Tang
              WPI; 2001-514838/56
                                                                        28-FEB-2000;
18-MAY-2000;
                                                                                                   26-FEB-2001; 2001WO-US04927
                                                                                                                           07-SEP-2001
                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                    (HYSE-) HYSEQ INC
                                                                                                                                               WO200164835-A2
                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                             06-NOV-2001
                                                                                                                                                                                                                                                                                                 AAO08818 standard; Protein; 99
                                                                                                                                                                                                                                       Human polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ JD No 11846; 1069pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                 Liu C,
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                                                                       2000US-0515126
2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Pred. No. 41;
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are used in
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Query Match
Best Local
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WPI; 2001-616774/71.
N-PSDB; AAS59607.
                                                         Skeiky YAW, Persing
L'maisonneuve J, Zh
                                                                                                                                                      21-APR-2000; 2000US-199047P
02-JUN-2000; 2000US-208841P
07-JUL-2000; 2000US-216747P
                                                                                                                                                                                                                                      20-APR-2001; 2001WO-US12865
                                                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                         01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                 WO200181581-A2
                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                           SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelltis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Propionibacterium acnes immunogenic protein #20799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU59903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU59903 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopoissis regulating activity, tissue growth factor activity, haematopoissis regulating activity, tissue growth factor activity, immunomodulatory activity and treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders
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                                                                               YAW,
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20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22710; 1399pp + Sequence Listing; English.
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                                                Mitcham JL, Wang
, Jen S, Carter I
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Pred. No. 66;
4; Mismatches
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CC polypeptides. The proteins and their associated DNA sequences are used in CC polypeptides. The proteins and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by CC p. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomylitis), weitis and endophthalmitis. CC pustulosis, hypertosis and osteomylitis), weitis and endophthalmitis. CC pustulosis, however it is particularly involved in the inflammatory CC nervous system, however it is particularly involved in the inflammatory CC lesions associated with acne vulgaris. A method for detecting the CC gresence or absence of p. acnes in a patient comprises contacting a CC presence or absence of p. acnes in a patient comprises contacting a CC gand determining the amount of bound protein in the sample. The CC and determining the amount of bound protein in the sample. The CC specific for P. acnes proteins. These antibodies can be used to convergulate expression and activity of P. acnes polypeptides and downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as therefore treat P. acnes infections. The antibodies may also be used as therefore treat P. acnes for determining P. acnes presence, for example, by diagnostic agents for determining P. acnes presence, for example, by diagnostic agents for data for this patent did not form part of the printed CC Note: The sequence data for this patent did not format directly from WIPO cat first the printed printed in electronic format directly from WIPO cat format directly from WIPO at first the printed printed as for this patent did not format directly from WIPO cat first active the printed at first active 
Search completed: April Job time: 75.037 secs
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                                                                                                                                                                                                                                                                                          δõ
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID No 21098; 1069pp; English.
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                                                                                                                                                                                             20 OPGHRRRGPVDGAHAHGIGGVRLLPAVP--LYAGLLAQLHRHRDRG 63
                                                                                                                                                                                                                                                                                          7 RPGSRARGNSSSNHLYGVAEAGAPPADPSTLYRDLPAEDSRGRQGG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.4%;
37.0%;
                                                                  4, 2003, 08:23:50
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Copyright

GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l number of hits satisfying chosen parameters:
    Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                    Score
  seq length: 40 seq length: 100
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1: /cgn2_6/ptodata/1.

2: /cgn2_6/ptodata/1.

3: /cgn2_6/ptodata/1.

4: /cgn2_6/ptodata/1.

5: /cgn2_6/ptodata/1.

6: /cgn2_6/ptodata/1.
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Gapop 10.0 ,
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  262574 seqs, 29422922 residues
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/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/ABCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
  DB
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                 US-08-973-544-4
US-08-379-538-2
US-08-379-538-3
US-08-379-538-3
US-08-685-871-63
US-08-685-871-63
US-08-685-871-63
US-08-799-173A-13
US-08-799-173A-13
US-08-905-223-44-44
US-08-905-223-15-20
US-08-905-223-44-40
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US-08-915-234-18-136
US-09-208-140-10
US-08-862-0218-18
PCT-US93-03164-20
US-08-862-0218-18
PCT-US93-03164-19
US-09-208-140-11
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       9, Appli
11, Appl
8, Appli
149, App
7, Appli
7, Appli
                                                                                                                             24, Appli

2, Appli

3, Appli

4, Appli

64, Appli

618, Appli

15, Appli

15, Appli

20, Appli

20, Appli

20, Appli

20, Appli

20, Appli
                                                                  21, Appl
21, Appl
18, Appl
18, Appl
11, Appl
11, Appl
12, Appl
7, ,
43,
108
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37.5	37.5	38	38	38	38	38	38.5	38.5	38.5	38.5	39	39	39	39	. u	ω 9	39
13.2	13.2	13.4	13.4	13.4	13.4	13.4	13.6	13.6	13.6	13.6	13.7	13.7	13.7	13.7	13.7	13.7	13.7
43	43 1	91 1	77 4	68	50 1	42 1	77 4	63 4	62	56 1	_	80 2				61 4	61 4
US-08-465-982-43	US-08-050-319B-43	US-08-469-202-18	US-09-605-785-558	US-08-484-434C-21	US-08-262-037-43	US-08-262-037-42	US-08-858-207A-285	US-09-099-631A-12	US-08-687-702-19	. US-08-538-165A-1		US-08-726-306A-173		US-09-444-295-108			US-09-135-010A-108
Sequence 43, Appl	Δ ω	18,	556	2	3	2	285	12	19	۲	20	17	. 10E	Sequence 108, App	Sequence 108, App	Sequence 108, App	Sequence 108, App

ALIGNMENTS

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; STRANDEDNESS:
; TOPOLOGY: lin
; MOLECULE TYPE:
US-08-973-544-4
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US-08-973-544-4
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                                                                                                                                                                                                          APPLICATION UNMER: US/08/973,544
FILING DATE: 18-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT EP 96/02663
FILING DATE: 20-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95109511.6
PRIOR APPLICATION NUMBER: EP 95109511.6
FILING DATE: 20-JUN-1995
PRIOR APPLICATION NUMBER: EP 95112201.9
FILING DATE: 03-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kitts, Monica Chin
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P8341-7073
TELECOMMUNICATION INFORMATION:
                                                                                                                                                     TELEFAX: (202)
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: WEISS, Elisabeth
TITLE OF INVENTION: NEW IMMUNOREGULATORY PROTEIN LST-1
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                     TELEFAX: (202) 638-4810
NFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20005-5701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
                                                                                     amino acid
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                                              linear
                                                                                                                                                                                                 (202)
                    protein
                                                                                                                                                                                                 638-5000
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Query Match

16.9%;

Score 48;

DB 4;

Length

97;

3 WACDCRARPL-WAWFORARVSSSDVTCATPPERQGRDLRALRE---ADFQAC 50

Matches

Local Similarity

36.5%;

Pred. No. 27;

Conservative

7;

Mismatches

16;

Indels

10;

Gaps

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RESULT 2
US-08-379-538-2
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Вb
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                                                              Matches
                                                              Best Local Similarity Matches 9; Conser
                                                                                           Query Match
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 573-1939
NFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Rele-
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 3-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                           MOLECULE TYPE: pi
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 573-4585
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US93/03921
FILING DATE: 30-APRIL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ronau, Robert T.
TITLE OF INVENTION: CALCIUM CHANNEL BLOCKING POLYPEPTIDES
TITLE OF INVENTION: FROM FILISTATA HIBERNALIS
                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 WAQGSSEQELHYASLQRLPVPSSE-----GPDLRGRDKRGTKEDPRADY-AC 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0 FILING DATE: 21-MAY-1992 APPLICATION NUMBER: PCT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
49
                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                           LENGTH:
                            5 CDCRARPLWAWFQRARVSSSDVTCATPPER 34
CKCD---
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: New York
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                                                                                                                                                                                                                                                                                          74 amino acids
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                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                           Filistata hibernalis
 WSWSQRIDDWRADYSCKCPEDQ 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfizer Inc
                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                     Bryan
                                                                               16.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                        34,462
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                                                                               Score 47;
Pred. No.
                                                                Mismatches
                                                                               DB 1;
27;
                                                                12;
                                                                                                Length 74;
                                                                 4.
                                                                   1:
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RESULT 3

Sequence 5, Application US/08379538 Patent No. 5804554

1:

GENERAL INFORMATION: APPLICANT: Volkman

APPLICANT:

Volkmann, Robert A. Saccomano, Nicholas A. Nason II, Deane M. Heck, Steven D.

Ronau,

APPLICANT:

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RESULT 4
US-08-379-538-5
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                                                                                                               Query Match
Best Local Similarity
'has 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 573-19 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Heck, Steven D.
APPLICANT: Ronau, Robert T.
TITLE OF INVENTION: CALCIUM CHANNEL BLOCKING POLYPEPTIDES
TITLE OF INVENTION: FROM FILISTATA HIBERNALIS
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 30-APRIL-19
ATTORNEY/AGENT INFORMATION:
NAME: Zielinski, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                         MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PC
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                                                                                                                                                                                                                                                               ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/8
EILING DATE: 21-MAY-1992
APPLICATION NUMBER: PCT/USS
EILING DATE: 30-APRIL-1993
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CITY: New York
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STREET: 235 East 42nd Street
                                                                49 CKCG----WSWSQRIDDWRADYSCKCPEDQ 74
                                                                                                                                                                                                            ORGANISM: F
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                              5 CDCRARPLWAWFQRARVSSSDVTCATPPER 34
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                                                                                                                                Conservative
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/ 10: 3:
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                                                                                                                                               Score 47;
Pred. No.
                                                                                                                                  Mismatches
                                                                                                                                                 DB 1; Length 74; 27;
                                                                                                                                  12;
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RESULT 5
US-08-379-538-4
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                                                                                                                                                                                               Sequence 4, Application Patent No. 5804554 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO ORIGINAL SOURCE:
                                                          CORRESPONDENCE ADDRESS:
                                                                                      TITLE OF INVENTION: CALCIUM CHANNEL BLOCKING |
                                                                                                                           APPLICANT:
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REFERENCE/DOCKET NUMBER: PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 573-4585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 30-APRIL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Z1611nski, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
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CORRESPONDENCE ADDRESS:
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                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 74 amino acids
TYPE: amino acid
TYPE: single
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 21-MAN APPLICATION NUMBER:
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                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                            CKCG----WSWSQRIDDWRADYSCKCPEDQ 74
                New York
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New York
                         E: Pfizer Inc
235 East 42nd Street
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                                                                                                                         Ronau, Robert T.
                                                                                                                                     Nason II, Deane M.
Heck, Steven D.
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                                                                                                                                                                     Saccomano, Nicholas A.
                                                                                                                                                                                    Volkmann, Robert A.
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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NO: 5:
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                                                                                                   CALCIUM CHANNEL BLOCKING POLYPEPTIDES
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                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 1; Length 74; Pred. No. 27;
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Query Match
Best Local Similarity
Watches 9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TISSUE TYPE: venom US-08-379-538-4
                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 63,
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-184102
FILING DATE: 25-JUN-1996
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Filistata hibernalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE N
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 07/887073
APPLICATION NUMBER: US 07/887073
FILING DATE: 21-MAY-1992
APPLICATION NUMBER: PCT/US93/03921
APPLICATION NUMBER: 907/US93/03921
FILING DATE: 30-APRIL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NARUMIYA, Shuh
APPLICANT: IWAMATSU, Akihiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                APPLICATION NUMBER: FILING DATE: 24-JUL CLASSIFICATION: 435
                                                                                                                                                                                                                                          STREET: 3000 K S
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 CKCG----WSWSQRIDDWRADYNCKCPEDQ 74
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SOFTWARE: Patenti
                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                          ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/
FILING DATE: 3-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08685871
                                                                                                                                                                                                                                                                       E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                        USA
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ilarity 30.0%;
Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                            UMBER: US/08/685,871
24-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 46; DB 1; Length 74; Pred. No. 36;
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

DATE:

14-SEP-1995

JP 7-262553

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                                                                                                                                                                                                                                                   RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 93
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                      GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZ010P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                           Sequence 618, Application US/09227357 Patent No. 6342581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
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                                                                                                                                                                                                                                                                                                                                                                            Matches
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APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT FILING DATE: 1998-04-27
CURRENT FILING DATE: 1998-04-27
RUMBER OF SEQ ID NOS: 38
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                  EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
                                                                                   CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
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REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
TYPE: amino acid
STRANDEDNESS: single
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NAME: BENT, Stephen A.
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5. 6348573
APPLICATION NUMBER: 60/052,793
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(202)672-5399
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36.4%;
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; TYPE: PRT; ORGANISM: Homo sapiens US-09-227-357-618
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EARLIER
Query Match
Best Local Similarity
Matches 12; Conserv
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FTI.TNG DATE: 1997-09-12
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APPLICATION NUMBER:
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27.3%;
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   Score 42.5; Di
Pred. No. 53;
2; Mismatches
                                  DB
                                  4;
                                  Length 41;
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Conservative

13;

Indels

17;

Gaps

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13 WAWFORARVSSSDVTCATPPEROGRDLRA-----LREADFQAC 50

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US-07-862-021B-20
                                                                                                                                                                                                                                               RESULT 10
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US-08-799-173A-13
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                                                                                                                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                        TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A NUMBER OF SEQUENCES: 20
                                                                                                                                                       APPLICANT: Jessell, Thomas M
APPLICANT: Klar, Avihu
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                       ADDRESSEE: Cooper & Dunham
STREET: 30 ROCKEFELLER Plaza
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HASTINGS, GREGG, APPLICANT: PATRICK J. DILLON
                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
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o. 5279966
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o. 5871969
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                                                                                                                                                                                                                                                                                                                                                                                                                    protein
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Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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                                                                                                                                                                                                                                                                                                                                                                   Length 53;
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PCT-US93-03164-20
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                TELEFAX: (212) 664-052
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application PC/TUS9303164 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
                                                                      NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                        APPLICATION NUMBER: PARTICING DATE: 19930402
                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza CITY: New York
                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 199204 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: AMINO ACID
STRANDEDNESS: Sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: White, John P
REGISTRATION NUMBER: 28,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CRMRPWTAWSECTKLCGGGI-----QERYMTVKKRFKSSQFTSC
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                                                                                                                                                                                                                                                                                                                                                                                                   10112
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55 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jessell, Thomas M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19920405
                                                               664-0525
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22.7%;
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                                                                                                                  40028
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Pred. No. 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
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US-08-905-223-444
                           20
                                                                                                                       US-08-905-223-444
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Best Local Similarity
Matches 10; Conserv
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                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                             Matches
                                                                                                                                                                                                                                                                                                                  TELEFAX: (619) 235-017
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: 5'
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: Win95
SOFTWARE: WORD
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                             MOLECULE TYPE: PROTEIN ORIGINAL SOURCE: ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Israelsen, Ned A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: AMINO ACID STRANDEDNESS: Si
                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CRMRPWTAWSECTKLCGGGI-----QERYMTVKKRFKSSQFTSC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 501 West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 CRARPLWAWFQRARVSSSDVTCATPPERQGRDLRALREADFQAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                    IDENTIFICATION METHOD: Von Heijne matrix OTHER INFORMATION: score 6.4 OTHER INFORMATION: seq SACLLLCPTWTNP/QL
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Israelsen, Ned A. REGISTRATION NUMBER: 29,655
                                                                                                                                                                                 NAME/KEY: sig_peptide LOCATION: -35...1
                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                            TOPOLOGY:
62
                             10 RPLWAW---FQRARVSSSDVTCATPPE 33
                                                                           Local Similarity
RPSXXWSLPYFRATVGSTEVSVAVTPD 88
                                                             10;
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                                                                                                                                                                                                                                                                                                       AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             California
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nilarity 22.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501 West Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lacroix, Bruno
VENTION: 5' ESTS FOR SECRETED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duelert, Aymeric
                                                                                                                                                                                                                                                                                                                         97 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                              Conservative
                                                                                                                                                                                                                                                                                        LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                    (619) 235-8550
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                                                                             15.0%;
37.0%;
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                                                                                                                                                                                                                                                                                                                                                           444:
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                                                             Score 42.5; DB 4;
Pred. No. 1.4e+02;
5; Mismatches 9;
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                                                                     Indels
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RESULT 13
US-09-208-140-10
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; ORGANISM: Viral
US-09-208-140-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09208140
Patent No. 6228576
GENERAL INFORMATION:
APPLICANT: Del Vecchio, Alfred
APPLICANT: Del Vecchio, Alfred
TITLE OF INVENTION: HEPARITIS C VIRUS NS5B TRUNCATED PROTEIN
TITLE OF INVENTION: AND METHODS THEREOF TO IDENTIFY ANTIVIRAL COMPOUNDS
FILE REFERENCE: P50743
CURRENT APPLICATION UNMBER: US/09/208,140
CURRENT FILING DATE: 1998-12-09
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 49
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US-08-444-818-136
                           ; MOLECULE TYPE: US-08-444-818-136
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Best Local Similarity 75.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6150087
                                                                                                                                                                                         PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US/08/403,590

FILING DATE: 14 -MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Harbin, Alisa A.

REGISTRATION NUMBER: 33,895

REGISTRATION NUMBER: 0110.002

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                     TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
CCLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Emeryville STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 ARPRWIWF 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 ARPLWAWF 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                      TOPOLOGY:
                                                                                        TYPE:
                                                                                                                                                                                TELEPHONE:
                                                                                                     LENGTH:
                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Chiron Corporation 4560 Horton Street
                                                                                                         60 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                              (508)359-3885
                                                                                                                                                                                  (508)359-3876
                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.4%;
14.48;
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Pred. No.
Score 41;
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1e+02;
 DB
   4.
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 Length 60;
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RESULT 15
US-09-047-125-21
Sequence 21, Application US/09047125
Patent No. 5976787
GENERAL INFORMATION: APPLICANT: Leland F. Velicer, Peter Brunovskis, TITLE OF INVENTION: Marek's Disease Herpesvirus CORRESPONDENCE ADDRESS: 34
CORRESPONDENCE ADDRESS: ADDRESSEE: Ian C. MCLEOd
STREET: 2190 Commons Parkway
Search completed: April 4, 2003, 08:26:06 Job time: 15.3333 secs
                                                                                 Ъ
                                                                                                              ş
                                                                                                                                                                                                            FEATURE:

NAME/KEY: Peptide of HSV1 gD polypeptide

LOCATION: 18 TO 216

OTHER INFORMATION: Peptide homologous to the US6 gene

US-09-047-125-21
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/736,335
FILING DATE: JULY 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. MCLECC
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-132
TELEPHONE: (517) 347-4100
TELEPAX: (517) 347-4103
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOTEOTICE TYPE: 11near
                                                                                                                                  Ouery Match 14.4%; Score 41; DB'2; Length 99; Best Local Similarity 27.1%; Pred. No. 2.3e+02; Matches 13; Conservative 7; Mismatches 24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb
COMPUTER: IBM PS2, Model 50
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: PC-Write 3.02
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,125
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 75.0 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide FRAGMENT TYPE: internal fragment ORIGINAL SOURCE:
                                                                               34
                                                                                     4 ACDCRARPLWAWFORARVSSSD----VTCATPPEROGRDLRALREADF 47
                                                                                                                                                                                                                                                                                                                   ORGANISM: herpes simplex virus type 1 (HSV1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Michigan
COUNTRY: USA
ZIP: 48864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 | ||
52 ARPRWIWF 59
                                                            ACPIRTOPRWNYYDSFSAVSEDNLGFLMHAPAFETAGTYLRLVKINDW 81
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Result
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Match Length DB
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Gapop 10.0 , Gapext 0.5
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284
1 NPWACDCRARPLWAWFQRAR......PPEROGRDLRALREADFQAC
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          Q64884 mouse adeno
Q98283 molluscum c
Q98283 molluscum c
Q13669 homo sapien
Q93db8 agrobacteri
Q00452 homo sapien
Q91un6 rizobium m
Q07301 pseudomonas
Q00454 homo sapien
Q91n99 lithobius f
Q9bgp8 macaca fasc
Q00453 homo sapien
Q9n698 xylella fas
Q09618 xylella fas
Q87603 chimpanzee
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ALIGNMENTS

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RESULT 2
Q9K3B9
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Q64884
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Best Local S
Matches 14
Q9K3B9 PRELIMINARY; PRT; 91 AA. Q9K3B9; 01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Putative redoxin. Putative redoxin. Screative Acc. Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q64884 PRELIMINARY; PRT; 100 AA.
Q64884;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
E3 class 1 protein.
Mouse adenovirus type 1 (MAV-1).
Viruses; dSDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-90177241; PubMed-2137954;
Beard C.W., Ball A.O., Wooley E.H., Spindler K.R.;

"Transcription mapping of mouse adenovirus type 1 early region
Virology 175:81-90(1990).

EMBL; M3395; AAM42494.1; ...

SEQUENCE 100 AA; 10908 MW; C8DDCC0E9C94BFA9 CRC64;
                                                                                                                                                                                           43
                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                               2 PWACDCRARPLW-----AWFQRARVSSSDVTCATPPERQGRDLRALR 43
                                                                                                                                                                                  PSQCQCPASPPWTNSSVTSFAQKTKWENSRQYCPVPSESSTRGKNAVR 90
                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                 20.1%;
                                                                                                                                                                                                                                              Score 57; DB:
Pred. No. 7.2;
6; Mismatches
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7.2;
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RESULT
Q98283
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RP RN
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"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces cocelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
                                                                                                                                                                                                                                                                                        iery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=A3(2);
Seeger K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-2000)
                                                                                                                                                                                                                                                                                                                                                                                                     Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Thomson N.R., James K.D., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borovok I., Karaffa L., Karaffa E., Cohen G., Aharon "Cloned Streptomyces coelicolor A3(2) operon encodin reductase reveals amino acid sequence high homology eukarytotic and viral ribonucleotide reductases."; submitted (MAR-2000) to the EMBL/GenBank/DDBJ databa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
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Cerdeno A.M., Parkhill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                 coelicolor A3(2).";

Nature 417:141-147(2002).

EMBL; A1359214; CAB94612.1;

EMBL; AJ276618; CAB82484.1;

SEQUENCE 91 AA; 9708 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=A3(2) / M145;
                                                                                                 01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                    Q98283
                                                                                                                                        Q98283;
                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence
                                              Molluscum contagiosum virus
Viruses; dsDNA viruses, no F
                                                                            MC116R.
SEQUENCE
                        NCBI_TaxID=10280;
                                     Molluscipoxvirus.
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                                                                                                                                                                                                                                                                                ocal
                                                                                                                                                                                                                                        NPWACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDLRALREADFQA
                                                                                                                                                                                                                 SPRTCRQCARPPWPGCHDVRASRSGPVDATPRALVSCPLPSLRRAPCRA
                                                                                                                                                                                                                                                                    l Similarity
17; Conser
                                                                                                                                                                                                                                                                                                                                                                                            D.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harris D.;
                                                                                                                                                      PRELIMINARY
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EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
                                                    subtype 1
RNA stage;
                                                     RNA
                                                                                                                                                                                                                                                                     Pred.
3; Mi
                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                             Score 52;
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                                                      (MCVI).
Poxviridae; Chordopoxvirinae;
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Senkevich T.G., Bugert J.J., Sisler J.R.,
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Q13669;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                Q93DB8 PRELIMINARY; PRT; 88 AA.
Q93DB8; Q93DB8; Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TREMBLREL. 21, Last annotation update)
01-JUN-2002 (TREMBLREL. 21, Last annotation update)
AvhB7 (Agrobacterium virulence homologue virB7).
AvhB7 OR ATUSI68 OR AGR_PAT_227.
AVHB7 OR ATUSI68 OR AGR_PAT_227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96006565; Pub
Holzinger I., de Baey
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 Agrobacterium tumefaciens Plasmid AT.
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IMBL; U00921; AAB57724.1; -.
                                 Agrobacterium tumefaciens,
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Catarrhini;
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Agrobacterium tumefaciens C58.";
Science 294.2323-2328(2001).
EMBL; AF396571; AAL04065.1;
EMBL; AE008940; AAL45858.1;
EMBL; AE007887; AAK90539.1;
                                                                                                                                                  01-JUL-1997
01-JUL-1997
01-DEC-2001
                                                                                                                                                                                           000452;
       SEQUENCE FROM N.A.
MEDLINE-98035883; PubMed-9367684;
de Baey A., Fellerhoff B., Maler
                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin Hountel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-A. tumefaciens (strain C58 / ATCC 33970); PLASHID-AT; MEDLINE-2160853; PubMed-11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen I., Chen Y., Wood D.W., Nester E.W.;
"A new type IV like secretion system promotes conjugal transfer cryptic plasmid of Agrobacterium tumefaciens.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-A.tumefaciens (strain C58 / MEDLINE-21608550; PubMed-11743193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Rhizobiaceae; Rhizobium.
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Primates;
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8; Mismatches
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Pred. No. 5
                                                                           Craniata; Vertebrata;
Catarrhini; Hominidae;
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                                                                                                                                                sequence u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                engineer Agrobacterium tumefaciens
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          Martinozzi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and biotechnology agent
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                                                                                                                                                                                                                                                                                                                                                       DB 16; Length
                                                                             Hominidae;
                                                                                                                                              update)
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        s.,
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        Weidle
                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                          88;
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01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                        SEQUENCE
                                                                  Plasmid
                                                                                                                                                     SEQUENCE FROM N.A.
TRANSPOSON-MERCURY RESISTANCE TRANSPOSON TN5718;
Schneiker S., Keller M., Droege M., Lanka E., Pu
                                                                                      Ptam;
                                                                                                      Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases EMBL; AJ304453; CAC79201.1;
                                                                                                                        "The genetic organization and evolution of mercury resistance plasmid pSB102 isolated residing in the rhizosphere of alfalfa.";
                                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                            PROSITE;
                                                                                                                                                                                                                                  Plasmid psB102
                                                                                                                                                                                                                                           Rhizobium meliloti
                                                                                                                                                                                                                                                               MerP protein
                                                                                              InterPro;
                                                                                                                                                                                                     NCBI_TaxID=382;
                                                                                                                                                                                                                 Rhizobiaceae;
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                                                                                                                                            "The genetic organization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complex expression pattern of the TNF region gene LST1 through differential regulation, initiation, and alternative splicing.", Genomics 45:591-600(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                     PF00403;
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sapiens 2,229,817bp
tted (SEP-1999) to th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF000424; AAB86998.1;
AF129756; AAD18090.1;
AP000505; BAB63394.1;
NCE 91 AA; 10133 MW
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19; Conserv
                  Similarity
9; Conser
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N., Dickhoff
                                                                          00403; HMA;
PS01047; H
                                                                                   IPR001934; HeavyMe_transpt
0403; HMA; 1.
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                                                        91 AA;
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1 (TrEMBLrel.
2 (TrEMBLrel.
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                  Conservative
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                                                                                                                                                                                                               Sinorhizobium
                                                                          HMA_1; UNKNOWN_1
                                                       9513 MW;
                                                                                                                                                                                                                                          (Sinorhizobium meliloti)
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                                                                                                                                                                                                                       alpha subdivision;
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genomic DNA of 6p21.3 HLA class
he EMBL/GenBank/DDBJ databases.
                 4.
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Last sequence update)
Last annotation updat
                         Score 47;
Pred. No.
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etz C., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Imai K., Shimada J.
EMBL/GenBank/DDBJ
                                                     BE988DE0405E79BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47.5;
                                                                                                                                                                                                                                                                                                               PRT;
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               Mismatches
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Madan
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22;
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n A., E
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                                                                                                                                 from a
                                                                                                                                           the broad-host-range
                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                    Rhizobiaceae group;
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Dors
                9
                                                                                                                                                             Puehler A.
                                 Length
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                Indels
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M., Young
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              Gaps
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11 PLWAWFQRARVSSSDVTCATPP

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01-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-Pseudomonas sp.; STRAIN-K-62;
MEDLINE-97311403; PubMed-9168120;
Kiyono M., Omura T., Inuzuka M., Fujimori H., Pan-Hou H.;
Riyono M., Omura T., Inuzuka M., Fujimori H., Pan-Hou H.;
"Nucleotide sequence and expression of the organomercurial-resistance determinants from a pseudomonas K-62 plasmid pMR26.";
Gene 189:151-157(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Mercuric transport protein periplasmic component precursor
(Periplasmic mercury ion binding protein) (Mercury scavenger protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-Pseudomonas sp. ED23-33; TRANSPOSON-TN5058; Minakhina S., Minakhin L., Kholodii G., Mindlin S., Gorlenko Z.H. Yurieva O., Nikiforov V.; "Molecular inventory of transposons from environmental bacteria: epidemic dissemination of Tn21-, Tn5041-, and Tn5053-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid pMR26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases. EMBL; D83080; BAA20336.1; . EMBL; Y17897; CAC14699.1; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Prote
NCBI_TaxID=306,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001934; HeavyMe_transpt.
InterPro; IPR001802; HG_scavenger.
Pfam; PF00403; HMA; 1.
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                                                                                                                                                                                                  01-JUL-1997 (TREMBLIEL 04, 01-JUL-1997 (TREMBLIEL 04, 01-DEC-2001 (TREMBLIEL 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P04129; 1AFJ
                                                                         Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                    000454;
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                                                                                                                                                                          LST1 protein.
  SEQUENCE FROM N.A
                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                          9
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9; Conservative
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                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9475 MW;
                                                                              Chordata; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19
91
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                                                                                                                                                                                                          Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47;
Pred. No.
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MERCURIC TRANSPORT PERIPLASMIC
A9EBA6234107596B CRC64;
                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                   PRT;
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.3e+02;
9;
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Best Local :
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Best Local
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                                                                                                             Q9BGP8 PRELIMINAKI,
Q9BGP8;
01-JUN-2001 (TrEMBLrel. 17; Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 9.9 kDa protein.
Macacca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Macacca fascicularis (Crab eating macaque) (Cynomolgus monkey).
The macacca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Macacca fascicularis (Crab eating macaque) (Cynomolgus monkey).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              differential regulation, in Genomics 45:591-600(1997). EMBL; AF000426; AAB87000.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Eukaryotic translation initiation factor 2 gamma (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Two genes become one: The genes encoding Heterochromatin protein sU(VAR)3-9 and translation initiation factor subunit eIF2gamma are joined to a dicistronic unit in holometabolic insects.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Myriapoda; Chilopoda; Pleurostigmophora; Lithobiomorpha; Lithobiidae; Lithobius. NCBI_TaxID=7552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9N9V9
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                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
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Osada N., Hida M., Kusuda J., Tanuma I
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ290958; CAB97508.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics 156:1157-1167(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Krauss V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lithobius forficatus
                                                                                NCBI_TaxID=9541;
                                                                                               Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Initiation factor.
                                                        SEQUENCE FROM N.A.
                                         TISSUE=FRONTAL LOBE LEFT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
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                                                                                                                                                                                                                                                                                                                      CDCRARPLWAWFQRARVSSSDVTCATPPERQG 36
                                                                                                                                                                                                                                                                                            CDCDACPRPACYRSAGSSKED---AFPCDRMG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                   l Similarity
13; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reuter
                                                                                                                                                                                                                                                                                                                                                                                                     80 AA;
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                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=11063691;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pattern of the TNF region gene LST1 through tion, initiation, and alternative splicing.";
                                                                                                                                                                                                                                                                                                                                                                                                        8902 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.4%;
39.0%;
                                                                                                                                                                                                                                                                                                                                                                16.4%;
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Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5A924968D231E74F CRC64;
                                                                                                                                                                                                                                                                                                                                                              Score 46.5; DB 5;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                          9F5463C25BBFBF06 CRC64;
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                              Tanuma R.,
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       from
                                                                                                                  vertebrata; Euteleostomi; i; Cercopithecidae;
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                               Iseki K., Hirai M.,
     macaque
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        CDNA
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                                    Terao
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Best Local
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775
033275
033275;
01-JAN-1998
01-JAN-1998
01-JAN-1998
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                                        Dasgupta N., Tyag1 J.S.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
EMBL; Y15717; CAA75732.1; -
SEQUENCE 99 AA; 10604 MW; 2768A2CD994D4D09 CRC64;
                                                                                                            Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                    STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                libraries.";
Submitted (FEB-2001) to the EM
EMBL; AR056424; BAB33082.1; -.
Hypothetical protein.
%FOUENCE 96 AA; 9903 MW;
                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    "Complex expression pattern of the TNF region gene LS differential regulation, initiation, and alternative Genomics 45:591-600(1997).

EMBL: AF000425; AAB86999.1; -.
SEQUENCE 97 AA; 10822 MW: AA03C761E787AF94 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997
01-JUL-1997
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-98035883; Pubme
de Baey A., Fellerhoff
Weiss E.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               lomo sapiens (Human).
                                                                                                                                                                                                                                                      56 YASLORLPVPSSE-----GPDLRGRDKRGTKEDPRADY-AC 90
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                Similarity
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16; Conserv
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(Tremburel.
        Conservative
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rhoff B., Maier S.,
              16.4%;
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Primates;
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39.0%;
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39.1%;
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19,
    Score 46.5; pred. No. 1.6e
5; Mismatches
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Last sequence update)
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Pred. No. 1.6e+
6; Mismatches
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                                       2768A2CD994D4D09 CRC64;
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Last annotation update)
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Pred. No. 1.6e
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                 AA03C761E787AF94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62E4A751F53B2E38 CRC64;
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                     DB
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    8
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                   Length 99;
  Indels
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RESULT 15
Q87603
ID 08760
AC 08760
DT 01-NO
DT 01-NO
DT 01-JU
DE Rev P
GN REV.
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RA Simpson A.JG., Relnach F.C., Arruda P., Abreu F.A., Acencio M., RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., RA Bueno M.R.P., Camaryo A.A., Camaryo L.E.A., Carraro D.M., Carrer H., RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M., Farnon M.C., Electro J.A., RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., RA Krieger J.E., Kuramae E.E., Laigret F., Lambeis M.R., Leite L.C.C., RA Machado M.A., Madeira A.M.S., Nadeira M.H., Marino C.L., Marques M.V., Martins E.A.L., Matrins E.M.F., Matsukuma A.Y., Marques M.V., Martins E.A.L., Matrins E.M.F., Matsukuma A.Y., RA Marques M.V., Martins E.A.L., Matrins E.M.F., Metto L.E.S., de Oliveira A.M., Nascimento A.L.T.O., Netto L.E.S., RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., A de Oliveira M.C., de Oliveira R.C., palmieri D.A., Paris A., Peixoto B.R., Roberto P.G., Rodrigues V., de ROSa A.J.M., RA Metto L.E., Silveira M.A., J.T., Nesquero J.B., RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Suwasaki H.E., RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., RE Lango M.A., Zatz M., Meidanis J., Setubal J.C., RT Truffi D., Santelli fastidiosa.", RE Endome Sequence of the plant pathogen Xylella fastidiosa.", BR Endone Sequence of the plant pathogen Xylella fastidiosa.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
Q9PDF8
                                                                                                                                                                                                                                                Matches
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Best Local
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                                       Q87603;
Q87603;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                            Hypothetical SEQUENCE 6
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01-OCT-2000
01-OCT-2000
01-MAR-2002
                                                                                                                                                                                                10 RPL-WAWFQRARVSSSDVTCATP---PEROGRDLRALREADFQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2371;
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                          protein
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                                                                                                                                                                       RPIVGRWEARLRLAGVSPHMATTDMRPLQQPKQSRYATEPDEAA
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15; Conserv
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                                    (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                        (Fragment).
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                                                                                                                                                                                                                                                                                                in; Complete proteome.
7178 MW; 2E1427E4525F7CD2
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34.1%;
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20,
                               Created)
Last sequence update)
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Pred. No. 1
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1.6e+02;
hes 20;
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Chimpanzee

immunodeficiency

virus

(SIV(cpz)) (CIV)

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OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RP STRAIN-P058;
RX MEDLINE-97138325; PubMed=8985351;
RX MEDLINE-97138325; PubMed=8985351;
RX MEDLINE-97138325; PubMed=8985351;
RX MEDLINE-97138325; PubMed=8985351;
RX Vidal N., Veas F., Durand J.P., Cuny G.;
RX Vidal N., Veas F., Durand J.P., Cuny G.;
RX Vidal N., Veas F., Durand J.P., Cuny G.;
RX Vidal N., Veas F., Durand J.P., Cuny G.;
RX Vidal N., Veas F., Durand J.P., Cuny G.;
RX Vidal N., Veas F., Durand J.P., Cuny G.;
RX Vidal N., Veas F., Durand J.P., Cuny G.;
RX Vidal N., Veas F., Durand J.P., Cuny G.;
RX Vidal N., Veas F., Durand J.P., Cuny G.;
RX Vidal N., Veas F., Durand J.P., Cuny G.;
RX Vidal N., Veas F., Durand J.P., Population immunodeficiency viruses from West
RY Populations from the same geographical locale.";
RX Vidal N., Veas F., Durand J.P., Population immunodeficiency viruses from West
RY Toll N., Veas F., Durand J.P., Population immunodeficiency viruses from West
RY Vidal N., Veas F., Durand J.P., Population immunodeficiency viruses from West
RY Toll N., Veas F., Durand J.P., Population immunodeficiency viruses from West
RY Toll N., Veas F., Durand J.P., Population immunodeficiency viruses from West
RY Toll N., Veas F., Durand J.P., Population immunodeficiency viruses from West
RY Toll N., Veas F., Durand J.P., Population immunodeficiency viruses from West
RY Toll N., Veas F., Durand J.P., Cuny J., Population immunodeficiency viruses from West
RY Toll N., Veas F., Durand J.P., Cuny J., Population immunodeficiency viruses from West
RY Toll N., Veas F., Durand J.P., Cuny J., Population immunodeficiency viruses from West
RY Toll N., Veas F., Durand J.P., Cuny J., Population immunodeficiency viruses from West
RY Toll N., Veas F., Durand J.P., Cuny J., Cuny J., Population immunodeficiency viruses from West
RY Toll N., Veas F., Durand J.P., Cuny J., Cuny J.
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Result
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Maximum Match 100%
Listing first 45 summaries
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score greater than
and is derived by a
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ster than or equal to the score of the result being printed,
rived by analysis of the total score distribution.
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2: /SIDS2/gcgdata/genesed/genesedp-embl/AA1981.DAT: *
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746.203 Million cell updates/sec
                                                          Novel human diagno
Partial human NgR3
Human PRO526 prote
                                                                                                                                                                                                                                                                                                                                                                                                              Description
                               Human PRO526
                                                                                                                                                                                                                                                                                 Human NgR2 protein
Mature human NgR2
                                                                                                                                                                                                                  Novel human diagno
Mouse NgR3 protein
                                                                                                                                                                                       Mature mouse
prote
(UNQ3
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TANGO 39 Nogo rec secreted secreted secreted secreted secreted secreted or or or secreted or or nanco 39 human di novel po human di novel po nyctalop nyctalop acid secreted secreted	Human PRO526 prote Human PRO526 antit Human PRO526 polyp Human Nogo recepto Human PRO526 prote Human PRO526 protectan Human PRO526 protectan Human PRO protein, Human secreted pro

ALIGNMENTS

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RESULT 1
AAO21477
ID AAO22
XX AAO2
AC AAO2
XX IS-A
XX Cere
KW NgR2
KW NgR2
KW Spir
KW Multy
KW Multy
KW Krat
KW Multy
KW Krat
KW Krat
KW Krat
KW Homc
KW FFT Regi
FT Regi
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                                                                                                                                                                                                                                Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologue; MyR2; NyR3; axonal growth; central nervous system; CNS; cerebral injury; spinal cord injury; stroke; demyelinating disease; multiple sclerosis; monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease; multifocal leukoencephalopathy; panencephalitis; Spongy degeneration; Alexander's disease; Canavan's disease; metachromatic leukodystrophy; krabbe's disease; immune; bait protein; genetic mapping; gene therapy; transgenic animal; unregulated cellular growth; cancer; tumour; human.
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                                Region
                                                                                              Region
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                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                           Human NgR2 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAO21477 standard; Protein; 420 AA
                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                       15-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA021477;
/label= 1
132..155
                                                              /label= LRR1_region
83..106
                           /label= LRR2_region
107. 131
                                                                                                                               /label= Signal_peptide 31..59
                                                                                                                                                                            Location/Qualifiers
                                                                                                         /label - LRRNT_region
             LRR3_region
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Region

/label= LRR4_region 156..179

'label= LRR5_region

203

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cc NgR3, comprising a 50 amino acid LRRCT sequence, a 284 amino acid with received consequence, or a 420, 461 or 392 amino acid sequence, all given in the specification. The NgR3 protein or as binding antibody is useful for cedecreasing inhibition of axonal growth of a central nervous system (CNS) neuron, by contacting the neuron NgR3 or its antibody, and for treating CC NS disease, disorder or injury. NgR3 or its antibody, and for treating cerebral injury, spinal cord injury, stroke, demyelination, encephalitis, multiple sclerosis, monophasic demyelination, encephaloguelitis, multiple sclerosis, monophasic cord englination, encephaloguelitis, multiple sclerosis, monophasic demyelination, encephaloguelitis, multiple sclerosis, monophasic cord assay, and as a research tool for inducing an immune response in a cord accord accordinate NgR3 is useful for inducing an immune response in a cord accordinate NgR3, as a bait protein in a two-hybrid or three-hybrid cord assay, and as a research tool for identification, characterisation and cord sequences of the invention are useful for screening for RFLP associated with certain disorders, for genetic mapping, and for gene therapy. The vector containing NgR3 is useful for producing non-human transgenic cord and therapeutic purposes. The sequences of the invention and cord and therapeutic purposes. The sequences of the invention, vectors and cord and therapeutic purposes. The sequences of the invention, vectors and cord and NgR2 protein of the invention.
(UYYA )
(BIOJ )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 injury, stroke, and demyelinating diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a Nogo receptor homologue polypeptide, NgR2 or NgR3, comprising a 50 amino acid LRRCT sequence, a 284 amino acid NTLRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 1; 277pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel Nogo receptor homolog polypeptide, NgR2 or NgR3, useful for treating central nervous system disorder, cerebral injury, spinal cord
Sequence
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BIOGEN INC
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MLPGLRRLLQAPASACULLMLLALPLAAPSCPMLCTCYSSPPTVSCQANNESSVPLSLPP 60

Matches Query Match

Local

Similarity

100.0%; ilarity 100.0%; Conservative

0;

Score 2226; DB 23; Pred. No. 4.7e-200; Mismatches

0;

Indels Length

Gaps

0;

420; 0;

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RESULT 2
AAO2146
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AAO2146
AC AAO2
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AC AAO2
XX
AC AAO2
XX
AC AAO2
XX
Cere
KW NgR:
KW NgR:
KW Mole
KW Krala
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WO2
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WO2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologum NgR2; NgR3; axonal growth; central nervous system; CNS; cerebral injur; spinal cord injury; stroke; demyelinating disease; multiple sclerosis; monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease; multifocal leukoencephalopathy; panencephalitis; Spongy degeneration; Alexander's disease; Canavan's disease; metachromatic leukodystrophy; Krabbe's disease; immune; bait protein; genetic mapping; gene therapy; transgenic animal; unregulated cellular growth; cancer; tumour; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mature human NgR2 protein sequence
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The invention relates to a Nogo receptor homologue polypeptide, NgR2 or NgR3, comprising a 50 amino acid LRRCT sequence, a 284 amino acid NTLRRCT sequence, or a 420, 461 or 392 amino acid sequence, all given in the specification. The NgR3 protein or its binding antibody is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-OCT-2001; 2001WO-US31488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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                                                                                                                                                                                    Novel Nogo receptor homolog polypeptide, NgR2 or NgR3, useful for treating central nervous system disorder, cerebral injury, spinal cord injury, stroke, and demyelinating diseases
                                                                                                                                                                                                                                                                                                                                                          Strittmatter SM, Cate
                                                                                                                                                                                                                                                                                                                                                                                                          (UYYA ) UNIV YALE. (BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALREADFQACPPAAPTRPGSRARGNSSSNHLYGVAEAGAPPADPSTLYRDLPAEDSRGRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALREADFQACPPAAPTRPGSRARGNSSSNHLYGVAEAGAPPADPSTLYRDLPAEDSRGRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLPGEALADLESLEFLRLNANEWACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDLR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSHLELHGNRLRLLTEHVERGLGSLDRLLLHGNRLQGVHRAAFRGLSRLTILYLFNNSLA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Page 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-238361P
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                                                                                                                                         277pp;
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                                                                                                                                                                                                                                                                                                                                                               Sah DWY;
                                                                                                                                            English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; Nogo receptor homologue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GC decreasing inhibition of axonal growth of a central nervous system (CNS) CC neuron, by contacting the neuron NgR3 or its antibody, and for treating CC CNS disease, disorder or injury, NgR3 or a vector comprising NgR3 is CC demyelinating diseases, e.g. multiple sclerosis, monophasic demyelinating, encephalomyelitis, multiple sclerosis, monophasic CC panencephalitis, Marchiafava-Bignami disease, Spongy degeneration, CC panencephalitis, Marchiafava-Bignami disease, Spongy degeneration, CC Reabbe's disease, Canavan's disease, metachromatic leukodystrophy and CC mammal against NgR3, as a bait protein in a two-hybrid or three-hybrid CC purlication of interacting, regulatory proteins. The nucleotide cequences of the invention are useful for screening for RFLP associated CC vector containing NgR3 is useful for producing non-human transgenic cand therapeutic purposes. The sequences of the invention and/or quantitation of NgR3, and for diagnostic CC and therapeutic purposes. The sequences of the invention, vectors and growth such as cancer and tumour growth. This sequence represents the mature human NgR2 protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
W0200175067-A2
                                     Homo
                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                  Novel human diagnostic protein #15164
                                                                                                                                                                                                                           ABG15173 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                                                                                           391
                                                                                                                                                                                                                                                                                                                                                                                                331 LYGVAEAGAPPADPSTLYRDLPAEDSRGRQGGDAPTEDDYWGGYGGEDQRGEQWCPGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 390; Consert
                                                                                                                                                                                                                                                                                                               QAPPDSRGPALSAGLPSPLLCLLLLVPHHL 390
                                                                                                                                                                                                                                                                                                                                    QAPPDSRGPALSAGLPSPLLCLLLLVPHHL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRGLVSLQYLYLQENSLLHLQDDLFADLANLSHLFLHGNRLRLLTEHVERGLGSLDRLLL 210
                                                                                                                                                                                                                                                                                                                                                                             LYGVAEAGAPPADPSTLYRDLPAEDSRGRQGGDAPTEDDYWGGYGGEDQRGEQMCPGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFOGLERLOSLHLYRCQLSSLPGNI 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRGLVSLQYLYLQENSLLHLQDDLFADLANLSHLFLHGNRLRLLTEHVFRGLGSLDRLLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         390 AA;
                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.5%;
                                                                                                                                                                                                                             807
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Pred. No. 1.4e-186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC a food supplement. (II) and its sunding partners are useful in medical conditions of sites expressing (II). (I) and (II) are useful for treating CC imaging of sites expressing (II). (I) and (II) are useful in medical conditions of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and CC consisted end polymorphic conditions are useful for the sequences and polymorphic conditions of the invention.

CC Note: The sequences are sequences of the invention.

CC antino acid sequences are discorders or other traits to assess biodiversity amino acid sequences of the invention.

CC specification, but was obtained in electronic format directly from MIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                509
                                                                                                                                                                                                                                                                                  457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                 HL-FLHGNRLRLLTEHVFRGLGSLDRLLLHGNRLOGVHRAAFRGLSRLTILYLFNNSLAS
                                                                                   LPGEALADLPSLEFLRLNANPWACDCRARPLWAWFORARVSSSDYTCATPPEROGRDLRA
                                                                                                                                                                                                EPDTFOGLERLOSLHLYRCQLSSLPGNIFRGLVSLQYLYLQENSLLHLQDDLFADLANLS
                                                                                                                                                                                                                                                                                                                                  LIRTLRPGTFGSNLLTLW------LFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSL
                                                               LPGEALADLPSLEFLRLNANPWACDCRARPLWAWFORARVSSSDVTCATPPERQGRDLRA
                                                                                                                                                                                                                                                                                                                                                                                                                 385;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID No 45532; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 807
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                    -GARHLWVQPAHPVALLQQPLHHL-PGHFPPLQALEELDLGDNRHLRSL
                                                                                                                                                                                                                                                                                                                                                                                                                            91.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1977.5;
Pred. No. 2.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                            DВ
                                                                                                                                                                                                                                                                                                                                                                                                       16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Length 807;
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                                                                 688
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362

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RESULT 4
AAO21478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologue; NgR2; NgR3; axonal growth; central nervous system; CNS; cerebral injury; spinal cord injury; stroke; demyelinating disease; multiple sclerosis; monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease; monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA021478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAO21478 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse NgR3 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           murine
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                                                                                                                                                                                          Region
        WPI; 2002-416677/44.
N-PSDB; AAL38334.
                                                            (UYYA )
                                                                                          06-OCT-2000; 2000US-238361P
                                                                                                                  06-OCT-2001;
                                                                                                                                                           WO200229059-A2
                                        Strittmatter SM, Cate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qs
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                                                             UNIV YALE.
BIOGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isease; immune; bait protein; genetic mapping; gene therapy; animal; unregulated cellular growth; cancer; tumour; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                   2001WO-US31488
                                                                                                                                                                                                                                                                                                                                                                                            /label= LRR1_region 93..106
                                                                                                                                                                                                                                                                                                                                                                                                                 /label= LRRNT_region
70..92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                /label= CTS_region
/note= "CT Signalling
439..462
/label= GPI_region
                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
                                                                                                                                                                                                                           321..438
                                                                                                                                                                                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                                                                                    42..165
                                                                                                                                                                                                                                                                                                                                                              'label= LRR3_region
                                                                                                                                                                                                                                                                            'label= LRR7_region
                                                                                                                                                                                                                                                                                                  'Label
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                                                                                                                                                                                                                                                                                                                      _= LRR5_region
                                                                                                                                                                                                                                                                                                                                                                                LRR2_region
                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal_peptide
                                           RL,
                                                                                                                                                                                                                                                                                                                                          LRR4_region
                                                                                                                                                                                                                                     LRRCT_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               461
                                            Sah DWY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΑA
                                                                                                                                                                                                      region"
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Novel Nogo receptor homolog polypeptide, NgR2 or NgR3, useful for treating central nervous system disorder, cerebral injury, spinal injury, stroke, and demyelinating diseases
                                                                                                                                                      cord
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cc quantitation, encephalitis, marchiarly mutitives, spongy degeneration.

Cc plexander's disease, Canavan's disease, metachromatic leukodystrophy and cc Alexander's disease, Canavan's disease, metachromatic leukodystrophy and cc krabbe's disease. NgR3 is useful for inducing an immune response in a cc mammal against NgR3, as a bait protein in a two-hybrid or three-hybrid cc says, and as a research tool for identification, characterisation and cc gequences of the invention are useful for screening for RFLP associated cc with certain disorders, for genetic mapping, and for gene therapy. The cc with certain disorders, for genetic mapping, and for gene therapy. The cc animals. The NgR3 binding antibody is useful for isolating and purifying canimals. The NgR3 binding antibody is useful for isolating and purifying cand therapeutic purposes. The sequences of the invention, vectors and cc antibodies are useful for treating or preventing unregulated cellular cc growth such as cancer and tumour growth. This sequence represents the cc mouse NgR3 protein of the invention. The invention relates to a Nogo receptor homologue polypeptide, NgR2 or NgR3, comprising a 50 amino acid LRRCT sequence, a 284 amino acid NTLRRCT sequence, or a 420, 461 or 392 amino acid sequence, all given in the specification. The NgR3 protein or its binding antibody is useful for specification in the NgR3 protein or its binding antibody is useful for decreasing inhibition of axonal growth of a central nervous system (CNS) neuron, by contacting the neuron NgR3 or its antibody, and for treating CRS disease, disorder or injury. NgR3 or a vector comprising NgR3 is CNS disease, disorder or injury, spinal cord injury, stroke, useful for treating cerebral injury, spinal cord injury, stroke, demyelinating diseases, e.g. multiple sclerosis, monophasic demyelination, encephalomyelitis, multifocal leukoencephalopathy, warning diseases and constraints and constraints are several constraints. NTLRECT

Query Match Best Local Similarity Matches 211; Conserv Conservative 40.98; 50; Score 911; DB 23; pred. No. 1.2e-76; 0; Mismatches 132; Length 461; 56; Gaps

12;

Sequence

461 AA;

οy Дb δÃ 밁 QΥ Вp δÃ В Qy Вb δÃ 밁 밁 316 306 256 246 196 186 136 126 11 433 374 346 76 66 17 APASAC---LLLMLLA--LPLAAPSCPMLCTCYSSPPTVSCQANNFSSVPLSLPPSTQRL FLONNLIRTLRPGTFGSNLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPD AQVSGCCVELLLLLLAGELPLGG-GCPRDCVCYPAPMTVSCQAHNFAAIPEGIPEDSERI CLAPLVALEFLRLNGNAWDCGCRARSLWEWLRRFRGSSSAVPCATPELRQGQDLKLLRVE ALADLESLEFLRLNANPWACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDLRALREA LHGNRLRLLTEHVFRGLGSLDRLLLHGNRLQGVHRAAFRGLSRLTILYLFNNSLASLPGE TFQGLVKLHALYLYKCGLSALPAGIFGGLHSLQYLYLQDNHIEYLQDDIFVDLVNLSHLF TFQGLERLQSLHLYRCQLSSLPGNIFRGLVSLQYLYLQENSLLHLQDDLFADLANLSHLF FLQNNRITFLQQGHFSPAMVTLWIYSNNITFIAPNTFEGFVHLEELDLGDNRQLRTLAPE DFRNCTGPVSPHQIKSHTLTTSDRAARKEHHPSH--GASRDKGHPHGHPPGSRSGYKKAG DFQACP-PAAP----PGAACQAPPDSRGPALSAGLPSPLLCLLL PSGVQQA--KNCTSHRN-RNQISKVSSGKELTELQDYAPDYQHKFSFDIMPTARPKRKGKCARRTPIRA ---TLYRDLPAEDSRGRQGGDAPTEDDYWGGY----TRPGSRARGNSSSNHLYGVAE----AGAPPADPS-----PLLAWIL 454 414 -GGEDQRGEQMC 75 65 315 185 135 125 255 245 195 345

RESULT 5 AAO21483

AAO21483 standard; Protein; 421

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CC The invention relates to a Nogo receptor homologue polypeptide, NgR2 or CC NgR3, comprising a 50 amino acid LRRCT sequence, a 284 amino acid NTLRRCT CC sequence, or a 420, 461 or 392 amino acid sequence, all given in the CC specification. The NgR3 protein or its binding antibody is useful for CC decreasing inhibition of axonal growth of a central nervous system (CNS) (CC cns disease, disorder or injury, NgR3 or a vector comprising NgR3 is demyelinating disease, e.g. multiple solerosis, monophasic demyelinating, encephalomyelitis, multifocal leukoencephalopathy, CC panencephalitis, Marchiafava-Bignami disease, Spongy degeneration, CC Alexander's disease, Canavan's disease, metachromatic leukodystrophy and CC assay, and as a research tool for inducing an immune response in a CC assay, and as a research tool for identification, characterisation and CC sequences of the invention are useful for screening for RFLP associated vector containing NgR3 is useful for producing non-human transgenic CC NgR3, for localisation and/or quantitation of non-human transgenic cand thorapeutic purposes. The sequences of the NgR3 and for diagnostic and thorapeutic purposes. The sequences of the invention are useful for isolating and purifying and thorapeutic purposes. The sequences of the invention, vectors and condition are useful for isolating and purifying antibodies are useful for treating or preventing unregulated cellular cc mature mouse NgR3 protein of the invention. This sequence represents the mature mouse NgR3 protein of the invention.
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     Ouery Match
Best Local Similarity
Matches 199; Conserv
                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 16; Page 106; 277pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel Nogo receptor homolog polypeptide, NgR2 or NgR3, useful for treating central nervous system disorder, cerebral injury, spinal injury, stroke, and demyelinating diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strittmatter SM, Cate
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                                                                                                       421
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                            39.8%;
Score 887; DB 23;
Pred. No. 1.9e-74;
9; Mismatches 126;
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49;

Length 421; Indels

50;

Gaps

9;

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RESULT 6
ABG15171
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation
                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                             N-PSDB; AAS79358
                                                                                                                                                                  Drmanac RT,
                                                                                                                                                                                         (HYSE-) HYSEQ
                                                                                                                                                                                                               31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                      WO200175067-A2
                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #15162.
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                                                                                                                                                                                                                                                                                                                                                     food supplement;
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                                                                                                                                         2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AWIL 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QDYAPDYQHKFSFDIMPTARPKRKGKCARRTPIRAPSGVQQA---SSGTALGA----PLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARGNSSSNHLYGVAE----AGAPPADPS-----TLYRDLPAEDSRGRQGGDAPTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLWAWFQRARVSSSDVTCATPPERQGRDLRALREADFQACP-PAAP-----TRPGSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARKEHHPSH--GASRDKGHPHGHPPGSRSGYKKAGKNCTSHRN-RNQISKVSSGKELTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDYWGGY - - .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HENQLQWVHHKAFHDLHRLTTLFLFNNSLTELQGDCLAPLVALEFLRLNGNAWDCGCRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGNRLQGVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLEFLRLNANPWACDCRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGGLHSLQYLYLQDNHIEYLQDDIFVDLVNLSHLFLHGNKLWSLGQGIFRGLVNLDRLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRGLVSLQYLYLQENSLLHLQDDLFADLANLSHLFLHGNRLRLLTEHVFRGLGSLDRLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFQGLERLQSLHLYRCQLSSLPGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CPMLCTCYSSPDTVSCQANNESSVPLSLPDSTQRLFLQNNLIRTLRPGTFGSNLLTLWLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPRDCVCYPAPMTVSCQAHNFAAIPEGIPEDSERIFLONNRITFLOOGHFSPAMVTLWIY
                                                                                                                                                                                                                                                                                                                                                                  chromosome
                                    SEQ ID No 45530; 103pp; English.
                                                                                                                                                               Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                   e mapping;
medical in
                                                                                                                                                               Tang
                                                                                                                                                                                                                                                                                                                                              j; gene mapping; gene therapy; forensic
imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GGEDQRGEQMCPGAACQAPPDSRGPALSAGLPSPLL
                                                                       mutations
o assess
                                                                                                                                                                                                                                                                                                                                                          forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321
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AAO21487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                          NgR2; NgR3; axonal growth; central nervous system; CNS; cerebral injury; spinal cord injury; stroke; demyelinating disease; multiple sclerosis; monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease; multifocal leukoencephalopathy; panencephalitis; Spongy degeneration; Alexander's disease; Canavan's disease; metachromatic leukodystrophy; Krabbe's disease; immune; bait protein; genetic mapping; gene therapy; transgenic animal; unregulated cellular growth; cancer; tumour; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Partial human NgR3 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAO21487 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 DDLFADLANLSHLFLHGNRLRLLTEHVFRGLGSLDRLLLHGNRLQGVHRAAFRGLSRLTI 231
                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                          Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERQGRDLRALREADFQACPPAAPTRPGSRARGNSSSNHLYGVAEAGAPPADPSTLY 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYLFNNSLASLPGEALADLPSLEFLRLNANPWACDCRARPLWAWFQRARVSSSDVTCATP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYLFUNSLASLPGEALADLPSLEFLRLNANPWACDCRARPLWAWFQRARVSSSDVTCATP 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                              /label=
101..124
                                                                                                        /label= LRR3_region
77..100
                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                  /Labe
                                                                                                                                                                                                       /label= LRR1_region
                                           /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuroprotective; cytostatic; Nogo receptor homologue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.6%;
91.0%;
                       ..148
                                                                 .124
                                                                                                                                                                    LRR2_region
                                                                                LRR4_region
    LRR6_region
                                           LRR5_region
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QY Вb

63

118 HLRSLEPDTFQGLERLQSLHLYRCQLSSLPGNIFRGLVSLQYLYLQENSLLHLQDDLFAD 177

LPPSTQRLFLQNNLIRTLRPGTFGSNLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNR 117 IPVDSERVFLQNNRIGLLQPGHFSPAMVTLWIYSNNITYIHPSTFEGFVHLEELDLGDNR 62

QLRTLAPETFQGLVKLHALYLYKCGLSALPAGVFGGLHSLQYLYLQDNHIEYLQDDIFVD

122

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Query Match Best Local Matches

al Similarity 51... 172; Conservative

40;

Mismatches

102;

22;

Gaps

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The invention relates to a Nogo receptor homologue polypeptide, NgR2 or NgR3, comprising a 50 amino acid LRRCT sequence, a 284 amino acid NTLRRCT sequence, a 284 amino acid NTLRRCT sequence, or a 420, 461 or 392 amino acid sequence, all given in the sequence, or a 420, 461 or 392 amino acid sequence, all given in the specification. The NgR3 protein or its binding antibody is useful for decreasing inhibition of axonal growth of a central nervous system (CNS) neuron, by contacting the neuron NgR3 or its antibody, and for treating CNS disease, disorder or injury, NgR3 or a vector comprising NgR3 is useful for treating cerebral injury, spinal cord injury, stroke, demyelinating disease, e.g. multiple sclerosis, monophasic demyelination, encephalomyelitis, multifocal leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease, Spongy degeneration, allexander's disease, Canavan's disease, metachromatic leukodystrophy and Krashe's disease, Canavan's disease, metachromatic leukodystrophy and Krashe's disease, Canavan's disease, metachromatic leukodystrophy and Krashe's disease, Incavally for information and immune reasonate in a
                                                                                   mammal against NgR3, as a bait protein in a two-hybrid or three-hybrid assay, and as a research tool for identification, characterisation and purification of interacting, regulatory proteins. The nucleotide sequences of the invention are useful for screening for RFLP associated with certain disorders, for genetic mapping, and for gene therapy. The vector containing NgR3 is useful for producing non-human transgenic animals. The NgR3 binding antibody is useful for isolating and purifying NgR3, for localisation and/or quantitation of NgR3, and for diagnostic and therapeutic purposes. The sequences of the invention, vectors and antibodies are useful for treating or preventing unregulated cellular growth such as cancer and tumour growth. This sequence represents the partial human NgR3 protein sequence of the invention.
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N-PSDB; AAL38335.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel Nogo receptor homolog polypeptide, NgR2 or NgR3, useful for treating central nervous system disorder, cerebral injury, spinal injury, stroke, and demyelinating diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strittmatter SM,
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                                                    Sequence
                                                          392 AA;
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/note= "CT Signalling region"
370..392
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173..196
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36.4%;
51.2%;
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Score 811;
Pred No.
    ; DB 23;
2.3e-67;
                    Length 392;
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RESULT 8
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28-APR-1999;
04-MAY-1999;
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10-MAR-1999;
12-MAR-1999;
23-MAR-1999;
12-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LANLSHLFLHGNRLRLLTEHVFRGLGSLDRLLLHGNRLGGVHRAAFRGLSRLTILYLFNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLKLLRAEDFRNCTGPASPHQIKSHTLTTTDRAARKEHHSPH--GPTRSKGHPHGPRPGH 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLRALREADFQACP-PAAP-----TRPGSRARGNSSSNHLYGVAEAGAPPADPSTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLSELQGECLAPLGALEFIRLNGNPWDCGCRARSLWEWLQRFRGSSSAVPCVSPGLRHGQ
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             99WO-US20111
99WO-US20594
99WO-US20944
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99WO-US21547
99WO-US23089
99WO-US23089
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99W0-US08615
99US-0131445
99US-0131425
99US-0134287
99US-0134287
99W0-US12252
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                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes sixty four human PRO proteins which can CC be used in the treatment of immune related diseases. The human PRO CC proteins, anti-PRO antibodies, agonists and antagonists are useful for CC treating and diagnosing immune related disorders. The disorders are CC estected from systemic lupus crythematosus, rheumatoid arthritis, selected from systemic lupus crythematosus, rheumatoid arthritis, constraints, juvenile chronic arthritis, spondyloarthropathies, constraints, systemic vasculitis, sarcoidosis, autoimmune haemolytic canaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, can peripheral nervous systems, hepatobiliary diseases of the central composed disease, gluten-sensitive enteropathy and whipple's disease, controlmune or immune-mediated skin diseases, allergic diseases, inflammatory constitution and controlmune or immune-mediated skin diseases, allergic diseases, controlmunological diseases of the lung, and transplantation associated controlmunological diseases and transplantation associated controlmunological diseases and transplantation probes used controlmunological diseases are described and hybridisation probes used controlmunological diseases are described and protein the present invention.
                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 191; Conserv
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                     195
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06-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ashkenazi AJ,
Kabakoff RC,
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TEHVFRGLGSLDRLLLHGNRLQGVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLE
                                                         TLHLDRCGLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHGNRISSV
                                                                                                                                     AASFRACRNLTILWLHSNVLARIDAAAFTGLALLEQLDLSDNAQLRSVDPATFHGLGRLH
                                                                            PGTFGS--NLLTLWLFSNNLSTIYPGTFRHLOALEELDLGDNRHLRSLEPDTFQGLERLQ 134
                                                                                                                                                                                                                VLWLQAWQVAAP-CPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRIFLHGNRISHVP
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DB; AAC58591.
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99WO-US28809
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2000WO-US00376
2000WO-US003441
2000WO-US04341
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Lu Y,
                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                              36.3%; Score 808; DB 21;
42.2%; Pred. No. 5.7e-67;
tive 38; Mismatches 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P, Goddard A, Gurney AL, Heb
an J, Pennica D, Shelton DL,
Watanabe CK, Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                  140;
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                                                                                                                                                                                                                                                                                              Indels
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DL, Smith
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98US-0080107

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98US-0080107

98US-0080327

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                                        09-APR-1998;
15-APR-1998;
15-APR-1998;
15-APR-1998;
15-APR-1998;
15-APR-1998;
21-APR-1998;
22-APR-1998;
22-APR-1998;
23-APR-1998;
23-APR-1998;
23-APR-1998;
29-APR-1998;
30-AMY-1998;
30-MAY-1998;
15-MAY-1998;
15-MAY-1998;
15-MAY-1998;
15-MAY-1998;
15-MAY-1998;
15-MAY-1998;
15-MAY-1998;
22-MAY-1998;
23-MAY-1998;
23-MA
                                                                                                                                                                                                                           New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders –  \frac{1}{2} \left( \frac{1}{2} \right) \left( \frac{1}{2} 
                                 The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation
                                                                                                                                                              Claim 12; Fig 161; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH )
                                                                                                                                                                                                                                                                                                                                                            1999-551358/46.
DB; AAZ34229.
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98US-008129
98US-0081838
98US-0081838
98US-0081952
98US-0082568
98US-0082568
98US-0082700
98US-0082700
98US-0082704
98US-0082704
98US-0082767
98US-0082767
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98US-0083495

98US-0083496

98US-0083590

98US-0083554

98US-0083554

98US-0083554

98US-0084414

98US-0084414

98US-0084411

98US-0084637

98US-0084637

98US-0084637

98US-0084637

98US-0085338

98US-0085338

98US-0085338

98US-0085338

98US-0085338

98US-0085338

98US-0085339

98US-0085339

98US-008538

98US-0085704

98US-0086414

98US-0086414

98US-0086410

98US-0086410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baker
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Best Local S
Matches 191
    08-MAR-1999;
12-MAR-1999;
29-MAR-1999;
21-APR-1999;
                                                                  18-FEB-2000; 2000WO-US04341.
                                                                                                                        WO200053756-A2
                                                                                                                                                                           expressed
                                                                                                                                                                                Human; secreted protein; transmembrane protein;
                                                                                                                                                                                                                 Human PRO526
                                                                                                                                                                                                                                            08-FEB-2001
                                                                                                                                                                                                                                                                       AAB44301;
                                                                                                                                                                                                                                                                                         AAB44301 standard; Protein; 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AA233891 to AA234338, and AA241685 to AA241774 represent polynucleotide and polypeptide sequence given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                   432
                                                                                                                                                                                                                                                                                                                                                                                                                      374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 SLHLYRCOLSSLPGNIFRGLVSLQYLYLGENSLLHLQDDLFADLANLSHLFLHGNRLRLL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 AASFRACRNLTILMLHSNVLARIDAAAFTGLALLEQLDLSDNAQLRSVDPATFHGLGRLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
                                                                                                                                                sapiens
                                                                                                                                                                                                                                                                                                                                                                                     GDAPTEDDYWGGYGGEDQRGEQMCPGAACQAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLRLNANPWACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDLRALREADFQAC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLHLDRCGLOELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHGNRISSY
                                                                                                                                                                                                                                                                                                                                                                 GOAGS----
                                                                                                                                                                                                                                                                                                                                                                                                            SGPRHINDSPFGTLPGSAEP--PLTAVRPEGSEPPGFPTSGPRRPPGCSRKNRTRSHCRL
                                                                                                                                                                                                                                                                                                                                                                                                                                       SS-NHL----YGVAEAGAPPADPSTLYR-----DLPAEDSRGRQG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPYHPIWTGRATDEEPLGLPKCCQPDAADKASVLEPGRPASAGNALKGRVPPGDSPPGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PTRPGSRAR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLRLNDNPWYCDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCAVAT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PERAFRGLHSLDRLLLHQNRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAPLRALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEHVFRGLGSLDRLLLHGNRLQGVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGTFGS--NLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFOGLERLQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLMLLALPLAAPSCPMLCTCYSSPP-TVSCQANNESSVPLSLPPSTQRLFLQNNLIRTLR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLWLQAWQVAAP-CPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRIFLHGNRISHVP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                         sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473 AA;
                                                                                                                                                                                                          (UNQ330) protein sequence SEQ ID
                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
99WO-USO5028.
99US-0123957.
99US-0126773.
99US-0130232.
                                                                                                                                                                                                                                                                                                                                                            -GGGGTGDSEGSGALPSLTCSLTP
                                                                                                                                                                         tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.3%;
                                                                                                                                                                        detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 808; DB 20;
Pred. No. 5.7e-67;
8; Mismatches 140;
                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                        cancer
                                                                                                                                                                                                                                                                                                                                                             459
                                                                                                                                                                                                                                                                                                                                                                                       394
                                                                                                                                                                                                             NO:400
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                                                                                                                                                                                  EST;
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                                                                                                                                                                                  cytostatic;
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Best Local Sim
Matches 191;
                                                                                                                                                                                                                                                                                                                                                                                                      AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bloactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bloactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-1999
14-MAY 1999
23-JUN-1999
26-JUL-1999
29-CCT-1999
30-NOV-1999
02-DEC-1999
02-DEC-1999
16-DEC-1999
16-DEC-1999
30-DEC-1999
30-DEC-1999
30-DEC-1999
30-DEC-1999
05-JAN-2000
06-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Fig 161; 636pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities -
                                                                                                                    194
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                                                                                                                                                                                                                                                                                                18 LLMLLALPLAAPSCPMLCTCYSSPP-TVSCQANNFSSVPLSLPPSTQRLFLQNNLIRTLR
GPYHPIWTGRATDEEPLGLPKCCQPDAADKASVLEPGRPASAGNALKGRVPPGDSPPGNG
                                                                    YLRLNDNPWYCDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCAVAT
                                                                                                                        TEHVERGLGSLDRLLLHGNRLQGVHRAAERGLSRLTILYLENNSLASLPGEALADLPSLE
                                                                                                                                                             TLHLDRCGLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHGNRISSV
                                                                                                                                                                             AASFRACRNLTILWLHSNVLARIDAAAFTGLALLEQLDLSDNAQLRSVDPATFHGLGRLH
                                                                                                        PERAFRGLHSLDRLLLHQNRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAPLRALQ
                                                                                                                                                                                                                                PGTFGS--NLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFQGLERLQ
                                                                                                                                                                                                                                                                         VLMLQAWQVAAP-CPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRIFLHGNRISHVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-611443/58.
DB; AAC78557.
                                                                                                                                                                                                                                                                                                                                                  Similarity
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1, Filvaroff E, Fong S, Gao W, Gerber H, Gerri
v, Godowski PJ, Grimaidi CJ, Gurney AL, Hillan
J, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA
L, Stewart TA, Tumas D, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                            473 AA;
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-US00219.
2000WO-US00277.
2000WO-US00376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0162506
99WO-US28313
99WO-US28551
99WO-US28565
99WO-US31095
99WO-US31274
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99US-0134287.
99US-0141037.
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                                                                                                                                                                                                                                                                                                                                                36.3%;
                             -----PPAA-----PTRPGSRAR----
                                                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                               Score 808; DB 21;
Pred. No. 5.7e-67;
88; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                          Length 473;
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eaton DL;
Gerritsen
                           -----GNS
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                                                                                                                                                                                                                                                                                                                               84;
 373
                                                     313
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                                                                                                          253
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RESULT 11
AAB24410
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26-JUL-1999;
01-SEP-1999;
08-SEP-1999;
13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; PRO; promotion; inhibition; at diagnosis; trauma; wound; cancer; atl angiogenic; proliferative; cardiant; cytostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO526 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07 - NOV - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB24410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB24410 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                     12-JAN-1999;
08-MAR-1999;
12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327
The present invention describes nucleic acids encoding PRO polypeptide useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the
                                                                                                                                                                              Godowski
Watanabe
                                                                                                                                                                                                                                                                                                                                             02-JUN-1999;
23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-NOV-1999;
                                                                                                 Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial angiogenic disorders in mammals -
                                                                                                                                                                                                  Ashkenazi AJ,
                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GOAGS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDAPTEDDYWGGYGGEDQRGEQMCPGAACQAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGPRHINDSPFGTLPGSAEP--PLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SS-NHL----YGVAEAGAPPADPSTLYR-----DLPAEDSRGRQG----
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                                                                                                                                                        2000-412154/35.
                                                                                                                                                                                                                                                                                                                                                                  ; 6661
                                                                                                                                               AAA77613
                                                                                                                                                                                                                         GENENTECH INC
                                                                                                                                                                              PJ,
                                                                             Fig
                                                                                                                                                                             , Baker KP,
Gurney AL,
Williams PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GGGGTGDSEGSGALPSLTCSLTP 459
                                                                                                                                                                                                                                                                             99US-0144758
99US-0145698
99WO-US20111
99WO-US20594
99WO-US20944
99WO-US21090
                                                                              46;
                                                                                                                                                                                                                                                                                                                                             99US-0134287.
99WO-US12252.
99US-0141037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US28313
                                                                                                                                                                                                                                                99US-0162506
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                                                                                                                                                                                                                                                                                                                                                                                                            98US-0112850
99US-0115554
                                                                             315pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                    -US05028
                                                                                                                                                                                                                                                                                                                                                                                      123957
                                                                                                                                                                                 PM,
                                                                               English.
                                                                                                                                                                                          Ferrara N,
Klein RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473
                                                                                                                                                                                  Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; angiogenesis; cardiovascularisation;
atherosclerosis; cardiac hypertrophy;
nt; cardiovascular; antiatherosclerotic;
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                                                                                                                                                                                             Kuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394
                                                                                                                                                                                            Gerber H,
Kuo SS, Pa
                                                                                                                                                                                             H, Hillan KJ,
Paoni NF, Sm
                                                                                                                                                                                                Smith
                                                            polypeptides
                                                                                                                                                                                                          Goddard A;
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or anglogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                       AAY95345
                                                                                          Key
                                                                                                                                          central
                                                                                                                                                                    pRO526; human;
breast cancer;
                                                                                                                                                                                                                                    25-SEP-2000
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                                                                                                                                                                                                          Human PRO526 antitumour protein.
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                                                                                                                Homo sapiens
Modified-site
                          Domain
                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                      432
                                                                                                                                                                                                                                                                                                                                                                              362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLHLYRCQLSSLPGNIFRGLVSLQYLYLQENSLLHLQDDLFADLANLSHLFLHGNRLRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGTEGS--NLLTLWLESNNLSTIYPGTERHLQALEELDLGDNRHLRSLEPDTEGGLERLO 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLWLQAWQVAAP-CPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRIFLHGNRISHVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLRLNDNPWVCDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCAVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLRLNANPWACDCRARPLWAWFORARVSSSDVTCATPPEROGRDLRALREADFQAC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPYHPIWTGRATDEEPLGLPKCCQPDAADKASVLEPGRPASAGNALKGRVPPGDSPPGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERAFRGLHSLDRLLLHQNRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAPLRALQ
                                                                                                                                                                                                                                                                                                                                                                            GDAPTEDDYWGGYGGEDQRGEQMCPGAACQAPP
                                                                                                                                                                                                                                                                                                                                                    GQAGS---
                                                                                                                                                                                                                                                                                                                                                                                                      SGPRHINDSPFGTLPGSAEP--PLTAVRPEGSEPPGFPTSGPRRPPGCSRKNRTRSHCRL
                                                                                                                                                                                                                                                                                                                                                                                                                              SS-NHL----YGVAEAGAPPADPSTLYR-----DLPAEDSRGRQG-
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                                                                                                                                            nervous
                                                                                                                                                         cancer;
                                                                                                                                                                                                                                                                                        standard;
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                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                           antitumour; tumour; therapy; cytostatic;
ovarian cancer; renal cancer; colorectal cance;
prostate cancer; lung cancer; bladder cancer;
s system cancer; melanoma; leukaemia; neoplasm.
                                                                                                                                                                                                                                                                                                                                                       -GGGGTGDSEGSGALPSLTCSLTP
                           /label= F
411..427
 /note=
82..86
                                                    /label= Signal_peptide 27..473
                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                         Protein;
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                "yon Willebrand factor
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                                         PRO526
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Pred. No. 5.7e-67;
8; Mismatches 140;
                                                                                                                                                                                                                                                                                            473 AA
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                                                                                                                                                                                                                                                                                                                                                                                  394
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                 type
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Matches
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Best Local
                                                                                                                                         The present sequence is that of human antitumour protein PRO526, as deduced from a foetal liver cDNA clone (see AAA49724). PRO526 has a mol.wt. of 50,708 and a pr of 9.28. It has homology to the leucine rich repeat protein superfamily. A claimed method for inhibiting the growth of a tumour cell comprises exposing the tumor cell pRO159, PRO2707, PRO3210, PRO2719, PRO2214, PRO324, PRO328, PRO301, PRO526, PRO362, PRO356, PRO599 or PRO866 (see AAY56337-49), their agonists or chimeric polypeptides incorporating them. The tumour is especially a cancer selected from breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder and central nervous system cancer, melanoma and leukaemia. Methods for the recombinant expression of the antitumour proteins are also provided.
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08-MAR-1999;
21-APR-1999;
28-APR-1999;
14-MAY-1999;
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26-JUL-1999;
15-SEP-1999;
                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                       Claim 19; Fig 18; 172pp; English.
                                                                                                                                                                                                                                                                                                                                       Novel composition to inhibit neoplastic cell growth or tumor in mammal comprises polypeptides PRO179, PRO207, PRO221, PRO324, PRO328, PRO301, PRO526, PRO362, PRO356,
                                                                                                                                                                                                                                                                                                                                                                                                                               Ashkenazi AJ, Goddard
Napier MA, Pitti RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-1999;
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                                       PGTFGS--NLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFQGLERLQ 134
                     VLWLQAWQVAAP-CPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRIFLHGNRISHVP 73
                                                                                                                                                                                                                                                                                                                                                                                             2000-442668/38.
DB; AAA49724.
                                                                             191;
                                                                         Similarity 42.2
91; Conservative
                                                                                                                             473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0131445.
99US-0134287.
99US-0144758.
99US-0145698.
99WO-US21090.
99WO-US21547.
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99WO-US05028.
99US-0130232.
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423..427
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372..376
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179..183
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45..51
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237..2
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110..116
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7..241
ASD 18
                                                                                     36.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "leucine zipper"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "glycosaminoglycan attachment site"
                                                                         38;
                                                                                                                                                                                                                                                                                                                                                                                                                              Godowski PJ,
i WI;
                                                                        Score 808; DB 21;
Pred. No. 5.7e-67;
8; Mismatches 140;
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                                                                                              Length 473;
                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                         PRO320, PRO219, PRO509 or
                                                                       84;
                                                                      Gaps
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RESULT: 13
AAU12362
ID AAU12362
XX AAU12362
XX AAU122
XX AAU122
XX DT 24-OC
XX Human
XW breas
XW carti
XW adipo
OS Homo
XX Homo
XX Homo
XX Homo
XX O1-DE
PR 01-DE
PR 01-DE
PR 02-DE
PR 10-DE
PR 10-DE
PR 10-DE
PR 11-FE
PR 11-FE
PR 11-FE
PR 11-FE
PR 11-FE
PR 22-FE
PR 22-FE
PR 21-MA
PR 21-MA
PR 21-MA
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  02-DEC-1999
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30-DEC-1999
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06-JAN-2000
11-FEB-2000
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11-FEB-2000
22-FEB-2000
24-FEB-2000
24-FEB-2000
24-FEB-2000
21-MAR-2000
21-MAR-2000
21-MAR-2000
21-MAR-2000
                                                                                                                                                                                                     01-DEC-1999;
01-DEC-1999;
02-DEC-1999;
02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                          Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                                                                                                          01-DEC-2000; 2000WO-US32678
                                                                                                                                                                                                                                                                                  07-JUN-2001
                                                                                                                                                                                                                                                                                                       WO200140466-A2
                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO526 polypeptide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU12362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPYHPIWTGRATDEEPLGLPKCCQPDAADKASVLEPGRPASAGNALKGRVPPGDSPPGNG
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2000WO-US00376
2000WO-US003565
2000WO-US04341
2000WO-US04414
2000WO-US04914
2000WO-US04914
2000WO-US05004
2000WO-US05501
2000WO-US05501
2000WO-US05501
2000WO-US07377
2000WO-US07373
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                                                                                                                                                        99US-0170262
99WO-US30095.
99WO-US30911.
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99WO-US31243
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                                                                                                                                                                                                      99WO-US28564
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*655555555555555555555555555555
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22-MAY-2000;
30-MAY-2000;
02-JUN-2000;
10-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Fig 382; 813pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baker KP,
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                                                                                                                                                                                                         TLHLDRCGLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHGNRISSV 193
                                                                                                                                                                                                                                                                              AASFRACRNLTILWLHSNVLARIDAAAFTGLALLEQLDLSDNAQLRSVDPATFHGLGRLH 133
                                                                                                                                                                                                                                                                                                             PGTFGS--NLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFQGLERLQ 134
                                                                                                                                                                                                                                                                                                                                                  VLWLQAWQVAAP-CPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRIFLHGNRISHVP 73
                                                                                                  FLRLNANPWACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDLRALREADFQAC----
                                                                                                                                       TEHVFRGLGSLDRLLLHGNRLQGVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLE
                                                                                                                                                                                                                             SLHLYRCOLSSLPGNIFFGLYSLQYLYLQENSLLHLQDDLFADLANLSHLFLHGNRLRLL 194
{\tt GPYHPIWTGRATDEEPLGLPKCCQPDAADKASVLEPGRPASAGNALKGRVPPGDSPPGNG}
                                                                   YLRLNDNPWVCDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCAVAT
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ME, Goddard A, Godows,
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2000WO-US14042.
2000WO-US14941.
2000WO-US15264.
2000WO-US30873.
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
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A, Godowski PJ, Gurney AL, Sh
Tumas D, Watanabe CK, Wood WI,
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8
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Pred.
                                      PPAA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                          808;
No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
.7e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                             140;
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L, Sherwood S
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               84;
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         373
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JAN-2000;
26-MAY-2000;
29-SEP-2000;
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                                                                                                                                                                               The sequence represents the human Nogo receptor, a protein expressed in axons and dendrites of neurons in the central nervous system during axonal growth. The invention relates to the use of the mogo receptor, nogo protein, their nucleic acids, vectors expressing them and artibodies against them, to isolate agents which block nogo receptor antibodies against them, to isolate agents which block nogo receptor mediated axonal growth. The agent is useful for treating a central nervous system disorder which is a result of cranial or cerebral trauma, spinal cord injury, stroke or a demyelinating disease selected from multiple sclerosis, monophasis demyelination, encephalomyelitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strittmatter
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                                                                multifocal leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration, Alexander's disease, Canavan's disease, metachromatic leukodystrophy, viral infection and Krabbe's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Page 89-90; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nervous system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel Nogo receptor protein useful for identifying modulator of Nogo protein or Nogo receptor protein, which is useful for treating centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYYA ) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQAGS-----GGGGTGDSEGSGALPSLTCSLTP
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DB; AASO9451.
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          473
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2000US-0207366.
2000US-0236378.
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          AA;
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Query Match
Best Local Similarity
Matches 191; Conserv

Conservative

38; Score Pred.

Mismatches No. 5.

DB 22; 5.7e-67; nes 140;

Length 473;

84;

Gaps

12;

36.3%;

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AABS0908
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  20-JUL-1999
28-JUL-1999
01-SEP-1999
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15-SEP-1999
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30-NOV-1999
90-DEC-1999
90-DEC-1999
20-DEC-1999
20-DEC-1999
10-JAN-2000
06-JAN-2000
11-FEB-2000
                                                                                                                                                                                                                                                              Human; PRO; antlinflammatory; dermatological; antlarthritic; antlineumatic; cardiant; antlanaemic; immunosuppressive; ant. antidiabetic; nootropic; neuroprotective; hepatotropic; viruantiallergic; antlasthmatic; immune related disorder; hepatobiliary disease; autoimmune disease; allergy.
                                                                                                                                                                                     02-JUN-2000;
                                                                                                                                                                                                                                WO200073452-A2
                                                                                                                                                                                                                                                                                                                                                                                                     AAB50908 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YLRLNDNPWYCDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCAVAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLHLDRCGLQELGPGLERGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHGNRISSV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLHLYRCQLSSLPGNIFRGLVSLQYLYLQENSLLHLQDDLFADLANLSHLFLHGNRLRLL 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLWLQAWQVAAP-CPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRIFLHGNRISHVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLMLLALPLAAPSCPMLCTCYSSPP-TVSCQANNESSVPLSLPPSTQRLFLQNNLIRTLR 76
99WO-US20111
99WO-US21147
99WO-US21547
99WO-US28313
99WO-US28313
99WO-US28634
99WO-US20911
2000WO-US00219
2000WO-US00376
2000WO-US00376
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99US-0144732.
99US-0144758.
99US-0146222.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC The present sequence is one of thirty three novel PRO polypeptides. CC The PRO polypeptides, anti-PRO antibodies, agonists and CC antagonists are useful for treating and diagnosing immune related CC disorders such as systemic lupus erythematosus, rheumatoid arthritis, constearthritis, juvenile chronic arthrilis, spondyloarthropathies, constead arthrilis, spondyloarthropathies, considering and commune thrombocytopaenia, thyroiditis, diabetes mellitus, considering and chronic arthrilis, spondyloarthropathies, sjoyren's considering and commune thrombocytopaenia, thyroiditis, diabetes mellitus, and peripheral nervous systems (such as multiple sclerosis, idiopathic considering polyneuropathy or Guillath-Barre syndrome, and chronic constraints of the contraints of the contraints of the contraints and infectious, autoimmune chronic active hepatitis, primary circhosis, granulomatous hepatitis and sclerosing cholangitis), considering disease, autoimmune crimmune-mediated skin diseases (such as bullous considered in diseases, such as sethma, allersitive enteropathy and whipple's skin diseases, such as asthma, allersic todermatitis, stopic dematitis, condact dermatitis, sporiasis), condact dermatitis, granultis, condact dermatitis, sporiasis), condact dermatitis, active and hypersensitivity and urticaria), immunological diseases of the condact dermatitis, active the condact dermat
                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                                         255
                                                                              194
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22-FEB-2000;
24-FEB-2000;
15-MAR-2000;
20-MAR-2000;
21-MAR-2000;
30-MAR-2000;
17-MAY-2000;
22-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashkenazi
Hebert C,
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 58; Fig 14; 218pp; English.
                                                                                                                                                                                                                                                                                                             18 LLMLLALPLAAPSCPMLCTCYSSPP-TVSCQANNESSVPLSLPPSTQRLFLQNNLIRTLR 76
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FLRLNANPWACDCRARPLWAWFQRARVSSSDVTCATPPEROGRDLRALREADFQAC----
                                                       PERAFRGLHSLDRLLLHQNRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAPLRALQ
                                                                                TEHVFRGLGSLDRLLLHGNRLQGVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLE
                                                                                                                                    TLHLDRCGLQELGPGLERGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHGNRISSV
                                                                                                                                                          AASFRACRNLTILWLHSNVLARIDAAAFTGLALLEQLDLSDNAQLRSVDPATFHGLGRLH
                                                                                                                                                                                                                                     PGTFGS--NLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFOGLERLQ
                                                                                                                                                                                                                                                                                         VLWLQAWQVAAF-CPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRIFLHGNRISHVP 73
                                                                                                                                                                                                                                                                                                                                                                                        191;
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DB; AAC91467.
                                                                                                                                                                                                                                                                                                                                                                               Similarity 42.2
91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                473
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Henzel W,
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2000WO-US04914
2000WO-US06884
2000WO-US06887
2000WO-US07377
2000WO-US07332
2000WO-US08439
2000WO-US13705
2000WO-US13705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
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Kabakoff
                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                       Score 808; DB 22;
Pred. No. 5.7e-67;
38; Mismatches 140;
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Shelton DL,
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Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                            Length 473;
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                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                               254
                                                                                                                                    193
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,	Sea	Db	Qy	Dр	Qy	ф	Qy	Db
	Search completed: April 4, 2003, 12:09:55 Job time : 77 secs	432		Db 374 SGPRHINDSPEGTLPGSAEPPLTAVRPEGSEPPGFPTSGFRKKEGCSKKKEGCSKKKEG		,		254 YLRLNDNPWVCDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAAN

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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775
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384
361
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341
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Gapop 10.0 , Gapext 0.5
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2226
1 MLPGLRRLLQAPASACLLLM.....LSAGLPSPLLCLLLLVPHHL 420
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sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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        09N0E3
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                                                                                                                                                                                                                                      SUMMARIES
Q9bzr6 homo sapien
Q99px18 mus musculu
Q99px18 mus musculu
Q99mx5 rattus norv
Q9ugs3 homo sapien
Q95139 homo sapien
Q90x15 homo sapien
Q90x16 homo sapien
Q90x16 mus musculu
Q8rzm3 rattus norv
Q90zx15 mus musculu
Q8rzg5 mus musculu
Q8rzg5 mus musculu
Q8rzg7 homo sapien
Q9qzu3 mus musculu
Q8rx113 mus musculu
Q8rx113 mus musculu
                                                                                                                                                             09n0e3 macaca fasc
Q9bzr6 homo sapien
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Q9N0E3

Q9N0E3 PRELIMINARY; PRT; 473 AA.
Q9N0E3;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)

308.5	309.5	310	310	311.5	312.5	312.5	312.5	315	315.5	317	317.5	319.5	319.5	320	321.5	325	326	326.5	326.5	329.5	330	331	331	331.5	333.5	334.5	337.5	2/1
13.9	13.9	13.9	13.9	14.0	14.0	14.0	14.0	14.2	14.2	14.2	14.3	14.4	14.4	14.4	14.4	14.6	14.6	14.7	14.7	14.8	14.8	14.9	14.9	14.9	15.0	15.0	15.3	1 5
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Q96jh3 homo sapien		_	Oswugs rattus norv			UZ4ZDU drosophila			U	Q92010 mus musculu	Q9Vu51 drosophila			omo	OSS rattus norv			-	Q93110 mus musculu	043300 homo sapien	macac	Quotes nomo sapien	nomo	- 1	Q9110W1 nomo sapien	homo	Q9dbb9 mus musculu	

ALIGNMENTS

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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,

RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,

RA Suzuki Y., Sugano S., Hashimoto K.;

RT Tisolation of full-length cDNA clones from macaque brain cDNA

RT Libraries.";

RT Libraries.";

RT Libraries.";

RT Libraries.";

RT Libraries.";

RR EMBL, AB045987; BAB01569.1;

DR EMBL; AB045987; BAB01569.1;

DR InterPro; IPR001372; LRR_Cterm.

DR InterPro; IPR000483; LRR_Cterm.

DR InterPro; IPR000372; LRR_Netrm.

DR InterPro; IPR003591; LRR_Typ.

DR Ffam; PF00560; LRR; B.

DR Pfam; PF01463; LRRCT; 1.

DR SMART; SM00013; LRRCT; 2.

SQ SEQUENCE 473 AA; 50644 MW; 53290DE83DB12CB3 CRC64;
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                                                                     Query Match
Best Local :
                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unnamed protein product.

Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutherla; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.
18 LLMLLALPLAAPSCPMLCTCYSSPP-TVSCQANNFSSVPLSLPPSTQRLFLQNNLIRTLR 76
                                                                   Similarity
                                                Conservative
                                    36.7%; Score 816; DB 6; Length 473; 42.6%; Pred. No. 4.1e-61; tive 36; Mismatches 140; Indels
                                  84;
                                Gaps
                                  12;
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42.2%;

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Query Match
                                                                                      Pfam; PF00560; LRR; 8.
Pfam; PF01463; LRRCT; 1.
SMART; SM00370; LRR; 3.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-21069055; PubMed-11201742;

FOURTHER A.E., Grandpre T., Strittmatter S.M.;

Macure 409:341-346(2001).
                                                                                                                                                                                                                            Interpro; IPR001611; I
Interpro; IPR000483; I
Interpro; IPR00372; I
Interpro; IPR003592; I
Interpro; IPR003591; I
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Q1.-JUN-2001 (TrEMBLrel. 17,
Q1.-JUN-2001 (TrEMBLrel. 17,
Q1-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                     TISSUB-LUNG;
Strausberg R.;
Strausberg R.;
Submitted (JUL-2001) to the EM
EMBL; AF283463; AAG53612.1; -.
EMBL; BC011787; AAH11787.1; -.
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                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGTFGS--NLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFQGLERLQ 134
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                                                    AΑ;
                                                    50707 MW;
                                                                                                                                                                                                                                                                                                                           LRR.
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           36.3%;
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           Score 808;
                                                       CA5624B24C584702 CRC64;
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                В
                4;
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              Length 473;
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Matches
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Q99PI8;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
                 InterPro: IPR003591; LRR_ty
pfam; pF00560; LRR; 8.
pfam; pF001463; LRRCT; 1.
SMART; SM00370; LRR; 5.
SWART; SM00082; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134
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                                                                                                                                                               STRAIN-SWISS-WEBSTER;
STRAIN-SWISS-WEBSTER;
MEDLINE=21069055; PubMed=11201742;
Fournier A.E., Grandpre T., Strittmatter S.M.;
Fournier A.E., Grandpre T., Strittmatter S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                               RTN4R
                                                                                                                                                                                                                                                                        Nogo receptor.
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                                                                                            Interpro; IPR001611;
Interpro; IPR000483;
Interpro; IPR000372;
                                                                                                                          EMBL; AF283462; AAG53611.1; MGD; MGI:2136886; Rtn4r.
                                                                                                                                              Nature 409:341-346(2001)
                                                                                                                                                       regeneration.
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                                                                                                                                                                                                       SEQUENCE FROM N.A
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SEQUENCE
                                                                                    InterPro; IPR003592;
          Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLMLLALPLAAPSCPMLCTCYSSPP-TVSCQANNFSSVELSLPPSTQRLFLQNNLIRTLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLWLQAWQVAAP-CPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRIFLHGNRISHVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERAFRGLHSLDRLLLHQNRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAPLRALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                GPYHPIWTGRATDEEPLGLPKCCQPDAADKASVLEPGRPASAGNALKGRVPPGDSPPGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191;
                                                                                                                                                                                                                                                                                                                                                                                         GDAPTEDDYWGGYGGEDQRGEQMCPGAACQAPP
                                                                                                                                                                                                                                                                                                                                                                                                            SGPRHINDSPFGTLPGSAEP--PLTAVRPEGSEPPGFPTSGPRRPGCSRKNRTRSHCRL
                                                                                                                                                                                                                                                                                                                                                                                                                             SS-NHL----YGVAEAGAPPADPSTLYR-----DLPAEDSRGRQG-----
                                                                                                                                                                                                                                                                                                                                                                         GQAGS---
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   473
                                                                                                                                                                                                                                                                                                                                                                         -GGGGTGDSEGSGALPSLTCSLTP
   AA;
                                                                                                                                                                                                                                      Chordata;
Rodentia;
    50987 MW;
                                                                                          LRR_out
                                                                               LRR_typ
                                                                                                   LRR_Nterm.
                                                                                                            LRR_Cterm.
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19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -PPAA-----PTRPGSRAR-----
                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                             PRT;
     14C5270EBF557E7C
                                                                                                                                                                                                                                                                                                                             473
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        CRC64;
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Length 473;

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                                                      C. STRAIN-SPRAGUE-DAWLEY;

ACT JIA W., Long M., Ju G.;

JIA W.-L., JIA W., Long M., Ju G.;

TIdentification and preparation of polyclonal antibody against rat vogo receptor.";

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL: AV028438; AAK20166.1; -.

RINTERPO: IPR001611; LRR.

PR InterPro: IPR001631; LRR.

INTERPO: IPR003592; LRR.

CU T.

RESMART: SM003592; LRR.

RESMART: SM003593; LRR.

RESMART: SM00369; LRR.

RESMART: SM00369; LRR.

RESMART: SM00369; LRR.

RECEPTOR: 473 AA; 50858 MW; FF87A6643F3A0A35 CRC64;
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     Ouery Match
Best Local Similarity
Matches 186; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                         Q99M75;
                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                    Nogo receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               432 GQAGS-----GASGTGDAEGSGALPALACSLAP 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLRLNDNPWYCDCRARPLWAWLQKFRGSSSEVPCNLPQRLADRDLKRLAASDLEGCAVAS
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       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
 34.2%; Score 762; DB 11;
41.1%; Pred. No. 1.6e-56;
tive 35; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.8%; Score 775; DB 11;
41.1%; Pred. No. 1.3e-57;
                                                                                                                                                                                                                                                                                                                                                                               17,
17,
18,
                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
, Last annotation update)
                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                     FF87A6643F3A0A35 CRC64;
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                          Length 473;
  Indels
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 84;
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Gaps
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12;
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RESULT 5
Q9GGS3
ID Q9GGS
AC Q9UG
AC Q9UG
AC Q9UG
DT 01-F
DE DJ7:
GN DJ
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R EMBL; AL035681; CAB63072.1; -.

R InterPro; IPR0001611; LRR.

IR InterPro; IPR000483; LRR_Cterm.

R InterPro; IPR000372; LRR_Mterm.

R InterPro; IPR0003592; LRR_out.

R InterPro; IPR003592; LRR_out.

R InterPro; IPR003592; LRR_tout.

R InterPro; IPR003591; LRR_typ.

Pfam; PP00460; LRR; 18.

Pfam; PP01463; LRRCT; 2.

R Pfam; PP01463; LRRCT; 2.

R PANAT; SM00019; LURRICHRPT.

SMART; SM00370; LRR.

SMART; SM00370; LRR.

SMART; SM00381; LRRCT; 2.

R SMART; SM00313; LRRCT; 2.

SMART; SM000369; LRR_TYP; 4.

PO SEQUENCE 797 AA; 85614 MW; 8C3247883EAE59AD CRC64;
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OSUGS3 PRT; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corby N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432
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2 LPGLRRLLQAPASACLLLMLLALP---LAAPSCPMLCTCYSSPPTVSCQANNESSVPLSL
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                                                                                                                       18.1%; ilarity 31.0%; Conservative 3
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                                                                                                               Score 402.5; DB 4;
Pred. No. 1.2e-25;
35; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          459
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                                                                                                                   184;
                                                                                                               Indels 103;
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                                 Query Match
Best Local S
Matches 154
                                                                             Interpro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 10.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01463; LERCT; 1.
SMART; SM00082; LRRCT; 1.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00313; LRRNT; 1.
SMART; SM00313; LRRNT; 10.
SMART; SM00369; LRR_TYP; 10.
SEQUENCE 811 AA; 88695 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                            075139
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01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                  075139;
                                                                                                                                                                                                                             code
                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                           KIAA0644
                                                                                                                                                                                                                                                                                                                                                                                      KIAA0644 protein.
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                                                                                                                                                                                                                                                                                                TISSUE=BRAIN
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                   MEDLINE=98403880; PubMed=9734811;
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                                                                                                                                                                      InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_
InterPro; IPR000372; LRR_
                                                                                                                                                                                                                  DNA Res.
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kes. 5:169-176(1998). 
AB014544; BAA31619.1; -.
LQAPASACLLIMI---LAL-PLAAPSCPMLCTCYSSPPTVSCQANNFSSVP--LSLPP--
                                 al Similarity
154; Conserv
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8 (TrEMBLrel.
1 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                  Conservative
                                                                                                                                                                                                                                                                                                                                           Chordata;
Primates;
                                                                                                                                                                                    LRR_Cterm
                                              17.3%;
28.3%;
                                                                                                                                                                      LRR_Nterm.
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                                     Score 384; DB 4;
Pred. No. 4.6e-24;
7; Mismatches 187
                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                 5741C766A8F75E78 CRC64;
                                                                                                                                                                                                                                                                           Miyajima
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Q9GZU5;
Q1-MAR-2001 (TrEMBLrel. 16, C
Q1-MAR-2001 (TrEMBLrel. 21, L
Q1-JUN-2002 (TrEMBLrel. 21, L
Leucine-rich repeat protein (
Bech-Hansen N.T., Nayhoum T.A., Sparkes R.L., Koop B., Birch D.G., Bergen A.A., Prinsen C.F., Polomeno R.C., Gal A., Drack A.V., Musarella M.A., Jacobson S.G., Young R.S., Weleber R.G., "Mutations in NYX, encoding the leucine-rich proteoglycan nyctalopin, cause X-linked complete congenital stationary night blindness."; Nat. Genet. 26:319-323(2000).

EMBL; AJ278865; CAC19014.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=110024/2, PubMed=110024/2, Pusch C.M., Zeitz C., Brandau O., Pesch K., Acuatz ..., Pusch C.M., Zeitz C., Brandau F.K., Pinckers A., Andreasst Scharfe C., Maurer J., Jacobi F.K., Pinckers A., Andreasst Hardcastle A., Wissinger B., Berger W., Meindl A., A., Wissinger B., Wissi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Pubmed=11062472;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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R INTERPRO; IPR0003591; LRR_Out.
R INTERPRO; IPR003591; LRR_Ctyp.
Pfam; pF01463; LRRCT; 1.
R Pfam; pF01463; LRRT; 1.
R Pfam; PF01463; LRRT; 1.
R SMART; SM00370; LRR; 6.
SMART; SM00082; LRRRT; 1.
R SMART; SM00082; LRRRT; 1.
R SMART; SM00013; LRRNT; 1.
R SMART; SM0005; LRR.Typ; 9.
R PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
SEQUENCE 481 AA; S1999 MW; 77855134DC564515 CRC64;
                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                            0944J0 PRELIMINARY; PRT; 495 AA.
0944J0; O1-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DJ16915.2 (novel leucine rich protein).
SEQUENCE FROM N.A Pavitt R.;
                                        NCBI_TaxID-9606;
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Interpro;
Interpro;
Interpro;
Interpro;
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                                                                                                                                                                                                                                                GVGGAGRQPWFLLASCLLPSVAQHV
                                                                                                                                                                                                                                                                         GPALSAGLPSPLL--CLLLLVPHHL 420
                                                                                                                                                                                                                                                                                                                         GAPPADPSTLYRDLPAEDSRGROGGDAPTEDDYWGGYGGEDQRGEQMCPGAACQAPPDSR
                                                                                                                                                                                                                                                                                                                                                     PGSVAGLDLSQVTFGRSSDGLCVDPEELNLTTSSPGPSPEPAATTVSRESSL----LSKL
                                                                                                                                                                                                                                                                                                                                                                                PPEROGRDLRAL------READFOACPPAAPTRPGSRARGNSSSNHLYGVAEA
                                                                                                                                                                                                                                                                                                                                                                                                              LHLNGNRLTVLAWVAFQPGFFLGRLFLFRNPWCCDCRLEWLRDWMEGSGRV--TDVPCAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADAFRGLRRLRTLNLGGNALDRVARAWFADLAELELLYLDRNSIAFVEEGAFQNLSGLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                       LRLNA------RPWACDCRARPLWAWFO-RARVSSSDVTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EHVFRGLGSLDRLLLHGNRLQGVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHLERGRIEAVASSSLOGLRRLRSLSLQANRVRAVHAGAFGDCGVLEHLLLNDNLLAELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HARTFAALSRLRREDLAACRLFSVPERLLAELPALRELAAFDNLFRRVPGALRGLANLTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPDTFQGLERLQSLHLYRCQLSSLP-------GNIFR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDLDRNGLRFLGERAFGTLPSLRRLSLRHNNLSFITPGAFKGLPRLAELRLAHNGDLRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLMLLALPLAAPS-----CPMLCTCYSSPP--TVSCQANNFSSVPLSLPPSTQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GLVSLQYLYLQENSLLHLQDDLFADLANLSHLFLHGNRLRLLT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFLONNLIRTLRPGTFGS--NLLTLWLFSNNLSTIYDGTFRHLQALEELDLGDNRHLRSL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVLLLHAVVLGLPSAWAVGACARACPAACACSTVERGCSVRCDRAGILRVPAELPCEAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 28.5
44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001064; Crystallin IPR001611; LRR.
                                                                                                                                                                                                                                                                                                     ----RVPVEEAANTTGGLA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.8%; Score 374; DB 4; 28.5%; Pred. No. 1.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38; M1smatches 185; Indels 138;
                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 481;
                                                                                                                                                                                                                                                                                                  NASLSDSLSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                            397
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RESULT
Q9DBY4
ID Q9
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Best Local S
Matches 142
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R Pfam; PF01463; LTRC; 1,

R Pfam; PF01463; LTRC; 1,

R Pfam; PF01463; LTRU; 1,

R SMART; SM00370; LTR; 6.

R SMART; SM00082; LTRCT; 1,

R SMART; SM00013; LTRNT; 1,

R SMART; SM00013; LTRNT; 1,

R SMART; SM00015; LTR_TYP; 9.

R SMART; SM00369; LTR_TYP; 9.
                                                              Q9DBY4;
Q9DBY4;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence up
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation
1200009022Rik protein.
                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                               Q9DBY4
                                                                                                                                                                                                               471
                                                                                                                                                                                                                                                                      438
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases EMBL; 293015; CAC16115.1; ... InterPro; IPR001064; Crystallin. InterPro; IPR001611; LRR. InterPro; IPR001631; LRR_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity es 142; Conserv
                                                                                                                                                                                                                            LPSPLL--CLLLLVPHHL
                                                                                                                                                                                                                                                                ----RVPVEEAANTTGGLA---
                                                                                                                                                                                                                                                                                  STLYRDLPAEDSRGROGGDAFTEDDYWGGYGGEDQRGEQMCPGAACQAPPDSRGPALSAG
                                                                                                                                                                                                                                                                                                             DLSQVTFGRSSDGLCVDPEELNLTTSSPGPSPEPAATTVSRFSSL----LSKLLAP----
                                                                                                                                                                                                                                                                                                                                                                 LTVLAWVAFQPGFFLGRLFLFRNPWCCDCRLEWLRDWMEGSGRV--TDVPCASPGSVAGL
                                                                                                                                                                                                              OPWFLLASCLLPSVAOHV
                                                                                                                                                                                                                                                                                                                                                                                                                     TEAVASSSLQGLRRLRSLSLQANRVRAVHAGAFGDCGVLEHLLLNDNLLAELPADAFRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GLVSLQYLYLQENSLLHLQDDLFADLANLSHLFLHGNRLRLLTEHVFRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSRLRRLDLAACRLFSVPERLLAELPALRELAAFDNLFRRVPGALRGLANLTHAHLERGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LERLQSLHLYRCQLSSLP------GNIFR-----GNIFR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLLALPLA-----APSCPMLCTCYSSPP--TVSCQANNFSSVPLSLPPSTQRLFLQNNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVLGLPSAWAVGACARACPAACACSTVERGCSVRCDRAGLLRVPAELPCEAVSIDLDRNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRFLGERAFGTLPSLRRLSLRHNNLSFITPGAFKGLPRLAELRLAHNGDLRYLHARTFAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRTLRPGTFGS--NLLTLWLFSNNLSTTYPGTFRHLQALEELDLGDNRHLRSLEPDTFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000372; LRR_Nterm.
IPR003592; LRR_out.
IPR003591; LRR_typ.
                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                      ---READFQACPPAAPTRPGSRARGNSSSNHLYGVAEAGAPPADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.6%;
                                                                                                                                                                                                              488
                                                                                                                                                                                                                                        420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 369; DB 4;
Pred. No. 4.6e-23;
8; Mismatches 184
                                                                                                                                           PRT;
                                                                                                                                           809
                                                                                                                                                                                                                                                             -----NASLSDSLSSRGVGGAGR
                                                                                    update)
on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 134;
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                                                                                                                                                                                                                                                                                                             437
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RA Kawai J. Shinagawa A. Shibata K. Yoshino M., Itoh M., Ishii Y., Ra Kawai J. Shinagawa A. Shibata K. Yoshino M., Itoh M., Ishii Y., Ra Arakawa T. Hara A. Fukunishi Y., Konno H., Adachi J., Fukuda S., Ra Arakawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ra Kadota K., Matsuda H., Riyosawa H., Kasukawa T., Saito R., Ra Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ra Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ra Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Ra Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Ra Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Ra Suzuki H., Toyo-oka K., Ringwald M., Rodriguez I., Sakanoto N., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Ra Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wilttaker C., Wilming L., Havshiraki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Вb
                                                                                                                                                                                                                                                                                                                                                                               Qγ
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Best Local (
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STRAIN-C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK004681; BAB23469.1; -.
EMBL; AK004681; BAB23469.1; -.
MGD; MGI:1914133; 120009022Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0019; LEURICHRPT.
SMART; SM00370; LRR; 8.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRWT; 1.
SMART; SM00369; LRR_TYP; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  136
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                   329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LALPLAAPS-CPMLCTCYSSPPTVSCQANNESSVP-LSLPPSTQ------
                                                                                                                                                                                                                                                                                                                                                                                                                    AFDFHRLGQLRRLDLQYNQIRSLHPKTFEKLSRLEELYLGNNLLQALVPGTLAPLRKLRI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAFPPRAESVCPERCDC-QHPQHLLCTNRGLRAVPKTSSLPSPQDVLTYSLGGNFITNIT
                                                                                                                                                                                                                                                                                                                                                                                 LDLGDNRHLRSLEPDTFQGLERLQSLHLYRCQLSSLPGNIFRGLVSLQYLYLQE-----
                                                                                                                                                            GVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLEFLRLNANPWACDCRARPL--WA
                                                                                                                                                                                                   LGLLSLSGNQLTHLAPEAFWGLEALRELRLEGNRLNQLPLTLLEPLHSLEALDLSGNELS
                                                                                                                                                                                                                                      LSHLFLHGNRLRLLTEHVFRGLGSLDRLLLHGNR-----
                                                                                                                                                                                                                                                                        {\tt GKNAFSQLGKLRFLNLSANELQPSLRHAATFVPLRSLSTLILSANSLQHLGPRVFQHLPR}
                                                                                                                                                                                                                                                                                                                                                LYANGN-EIGRLSRGSFEGLESLVKLRLDGNVLGALPDAVFAPLGNLLYLHLESNRIRFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00560; LRR; 10.
PF01463; LRRCT; 1
                                                    GNWHSQGRLLTVFVQCRHPPALRGKYLDYLDDQLLQNGSCVDPSPSPT-AGSRQWPLPTS
                                                                                                                           ALHPATEGHQGRLRELSLRDNALSALSGDIFAASPALYRLDLDGNGWTCDCRLRGLKRWM
NHLYGVAEAGAPPADPSTLYRDLPAE-----DSRGR-QGGDAPTEDDYWGGYGGEDQRGE
                                                                                     --WFQRARVSSSDVTCATPPERQGRDLRALREADFQ--AC--PPAAPTRPGSRARGNSSS 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000372; LRR_Nterm.
IPR003592; LRR_out.
IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.2%;
nilarity 28.9%;
Conservative 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            809 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----RLFLQNNLIRTLRPGTFG--SNLLTLWLFSNNLSTIYPGTFRHLQALEE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=LUNG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88809 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            score 361.5; DB pred. No. 3.7e-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5E86F55B8AE419FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11;
                                                                                                                                                                                                                                                                                                                     -----NSLLHLQDDLFADLAN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 809;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                164
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                                                                                                                                                                              274
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ORESWITH
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                                                                                                                                                                                                                                                                                                                                  RESULT
Q9CZT5
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STRAIN=WISTAR RATS; TISSUE-BRAIN;
STRAIN=WISTAR RATS; PubMed=11785964;
MEDLINE=21645900; PubMed=11785964;
Satoh K., Hata M., Yokota H.;
"A Novel Member of the Leucine-Rich Repeat Superfamily Induced "A Novel Member of the Leucine-Rich Repeat Superfamily Induced Astrocytes by beta-Amyloid.";
Astrocytes by beta-Amyloid.";
Biochem. Biophys. Res. Commun. 290:756-762(2002).
Biochem. Biophys. Res. Commun. 991:56-762(2002).
EMBL; AB071036; BAB84586.1; -.
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01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                            Q9CZT5 PRELIMINARY;
Q9CZT5;
Q1-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
2610528605Rik protein.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat)
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                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                      2610528G05RIK.
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Rodentia;
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                                                                                                                                                                                         Last sequence update)
Last annotation updat
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Sciurognathi; Muridae; Murinae; Rat
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                                      Craniata; Ver
Sciurognathi;
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                                         Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
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RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peeole G., Quackenbush J.,
RA Schriml L.M., Stabbli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Stabbli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schei K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibate Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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Pfam: PF01462; LRRT; 1.
PRINTS; PR00019; LEUTIHRPT.
SMART; SM00001; EGF; 1.
SMART; SM00001; EGF_11ke; 1.
SMART; SM000070; LRRCT; 1.
SMART; SM00082; LRRCT; 1.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
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InterPro: IPR000561; EGF-11ke.
InterPro: IPR003961; FN_III.
InterPro: IPR001611; LRR.
208 LLLHGN-RLQGVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLEFLRLNANPWACD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK012169; BAB28075.1; -.
HSSP; P00740; IEDM.
                                                                                                                                                                     155
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SEQUENCE FROM N.A.
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                                                                                    ILDTANVEALRLAGLGLRQLDEGLFGRLLNLHDLDVYDNQL----EHMPSVIQGLRGLTR
                                                                                                                                                                                                    LYLGKNR-IRHIQPGAFDALDRLLELKLPDNELRVLPPLHLPRLLLLDLSHNSIPALEAG
                                                                                                                                                                                                                                      LDLGDNRHLRSLEPDTFQGLER------LQSLHLYRCQLSSLPGNIFRGL---
                                                                                                                                      ···-VSLQYLYLQENSLLHLQDDLFADLANLSHLFLHGNRLRLLTEH---VFRGLGSLDR
                                                                                                                                                                                                                                                                                                                       VGCFAGLPGLQLLDLSQNQITSLPGGIFQPLVNLSNLDLTANKLHEISNETFRGLRRLER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00022; EGF_1; UNKNOWN_1.
PS01186; EGF_2; 1.
673 AA; 72336 MW; 9C53
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; IPR003592;
; IPR003591;
00008; EGF; 1
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LRR_Nterm.
LRR_out.
LRR_typ.
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Fukuda S.,
manaka I.,
Saito R.,
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Q8R2G5
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Best Local
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE STRAIN-C57BL/6;
STRAIN-C57BL/6;
Kutejova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
364 STIREPTLSTSSQAPTWPSLTEPTTQASTVLSTAPPTMRPAPQPQDCPASICLNGGSCRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases EMBL; AJ458938; CAD30331.1; -.
                                                                                                                                                                              189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schrewe H., Kutejova E.;
"Structure and expression analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                 70 VGCFAGLPGLQLLDLSQNQITSLPGGIFQPLVNLSNLDLTANKLHEISNETFRGLRRLER
                                                                                                                                                                                                                                                                                                                                       11 LLLLLVLLGSGVQGCPSGCQC-NQPQTVFCTARQGTTVPRDVPPDTVGLYIFENGITTLD
                                                                                                                                                                                                                                                                                                                                                        17 LLLMLLALPLAAPSCPMLCTCYSSPPTVSCQANNFSSVPLSLPPSTQRLELQNNLIRTLR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424
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                                                                                                                             LLLHGN-RLQGVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLEFLRLNANPWACD
                         PGSRARGNSSSNHLYGVAEAGAPPADPSTLYRDLPAEDSRGRQGGDAPTEDDYWGGYG--
                                                     CPLSWFGPWVRENHVVLASPEETRCHFPPKNAGRLLLDLDYADF-GCPVTTTTATVPTIR
                                                                               CRARPLWAWFQRARV----SSSDVTCATPPERQGRDLRALREADFQACPPAAPT-----R
                                                                                                             LRLAGNTRIAQIRPEDLAGLTALQELDVSNLSLQALPSDLSSLFPRLRLLAAARNPFNCL
                                                                                                                                                                  ILDTANVEALRLAGLGLRQLDEGLEGRLLNLHDLDVSDNQL----EHMPSVIQGLRGLTR
                                                                                                                                                                                                                          LYLGKNR-IRHTQPGAFDALDRLLELKLPDNELRVLPPLHLPRLLLLDLSHNSIPALEAG
                                                                                                                                                                                                                                                    LDLGDNRHLRSLEPDTFQGLER-----
                                                                                                                                                                                             ----VSLQYLYLQENSLLHLQDDLFADLANLSHLFLHGNRLRLLTEH---VFRGLGSLDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGSRARGNSSSNHLYGVAEAGAPPADPSTLYRDLPAEDSRGRQGGDAPTEDDYWGGYG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEDQRGEQMCP----GAACQAP-----PDSRGPALSAGLPSPLLCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STIREPTLSTSSQAPTWPSLTEPTTQASTVLSTAPPTMRPAPQPQDCPASICLNGGSCRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRARPLWAWFQRARV----SSSDVTCATPPERQGRDLRALREADFQACPPAAPT-----R
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673 AA;
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673 S
72261 MW;
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29.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 356.5;
Pred. No. 7.8
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SLIT-LIKE 2 PROTEIN.
AAB8DA82DA8E9D32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                      sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                  89;
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                                                                                                                                       266
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GAACQAP------PDSRGPALSAGLPSPLLCL 412

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RESULT
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SQ
RESULT 14
Q99ZU3
ID Q99ZU
AC Q99ZU
AC Q99ZU
DT 01-M2
DT 01-M2
DT 01-JU
DE Plate
GN MUS 1
OC EUkan
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OC Mamme
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Best Local (
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O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Insulin-like growth factor binding protein, acid labile subunit.
Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8TAY0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC025681; AAH25681.1; .
SEQUENCE 605 AA; 66066 MW; F6527A23CBE218F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=LUNG
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                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Platelet glycoprotein V (Fragment)
                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                                                                                                                                                          Q9QZU3
 SEQUENCE
                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                              467
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                                                                                                                                                                                                                                                                                                                                                                                                                     408
                                                                                                                                                                                                                                                                                                                                                                                                                                                201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLSSLPGNIFRGLVSLQYLYLQENSLLHLQDDLFADLANLSHLFLHGNRLRLLTEHVFR 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --NLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFQGLERLQSLHLYR 140
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                                                                                                                                                                                                                                                                                                                                                           RNRLAELPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNNSLRTFTPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                   GLSGLRRLFLKDNGLVGIEEQSLWGLAELLELDLTSNQLTHLPHR-LFQGLGKLEYLLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                GLGSLDRLLLHGNRLQGV--------HRAAFRGLSRLTILYLF
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                                                                                                                                                                                                                                                                                                      GLERLWLEGNPWDCGCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPAYTYNNITCASP
                                                                                                                                                                                                                                                                                                                                   SLEFLRLNANPWACDCRARPLWAW----
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    FROM
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                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                 605
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Pred. No. 2
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                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Murinae; Murinae;
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                                                 Mus.
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Interpro; IPR001611; LRR.
Interpro; IPR000483; LRR_Cterm.
Interpro; IPR000372; LRR_Out.
Interpro; IPR003592; LRR_out.
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Ministri-Madrid K., DuBridge R.B., Phillips D.R.;
"Increased thrombin responsiveness in platelets from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycoprotein V.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20027548; PubMed-10557321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00560; LRR; 13
Pfam; PF01463; LRRCT;
                                                                        OSDITO PRELIMINARY: PRF: 614 AA.

OSDITO:
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TREMBLrel. 17, Last sequence update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
Adult male testis cDNA, RIKEN full-length enriched clone:4930471K13, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                    Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 NQLSFLPANLFSSLRELKLLDLSRNNLTH-LPKGLLGAQVKLEKLLLYSNQLTSVDSGLL
                         NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                FENPLEELPDYLFGEMAGLRELWLNGTHLSTLPAAAFRNLSGLQTLGLTRNPRLSALPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNLGALTELRL-ERNHLRSVAPGAFDRLGNLSSLTLSGNLLESLPPALFLHVSSVSRLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHLQALEELDLGDNRHLRSLEPDTFQGLERLQSLHLYRCQLSSLPGNTFRGLVSLQYLYL
                                                                                                                                                                                                                                      YRDLPAEDSRGRQGGDAPTEDDYWGGY 374
                                                                                                                                                                                                                                                                 CRGPEPRASLSFWELLQGD-PWCPD-----PRSLPLDPPTENALEAPVPSWLPNSWQSQT
                                                                                                                                                                                                                                                                                       RQGRDLRA-----LREADFQACPPAAPTRPGSRARGNSSSNHLYGVAEAGAPPADPSTL
                                                                                                                                                                                                                                                                                                                LEHNQLETLPGDVFAALPQLTQVLLGHNPWLCDC---GLWPFLQWLRHHPDILGRDEPPQ
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119; Conservative
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; SM00369; LRR
567
NCE 567 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B2; LRR; 2.
82; LRRCT; 1.
13; LRRNT; 1.
9; LRR_TYP; 10.
7
867
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AA:
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                                       Chordata;
Rodentia;
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                                        sciurognathi;
                                                      Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E6AF470855ACB6C9 CRC64;
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                                        Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
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RA Alzawa K., Izawa M., Nishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi R., Riyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi R., Riyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi R., Riyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Gustincich S., Hill D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Lyons P., Marchionni L., Mashina M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Havashizaki Y.:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 15.4%; Score 343; DB 11; Length 614; Best Local Similarity 28.5%; Pred. No. 9.8e-21; Matches 115; Conservative 50; Mismatches 133; Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.
Pfam; PF00560; LRR; 9..
Pfam; PF01463; LRRCT; 1.
Pfam; PF01462; LRRNT; 1.
SMART; SM00409; IG; 1.
SMART; SM00409; IGc2; 1.
SMART; SM00410; IG_1ike; 1.
SMART; SM00081; LRRCT; 1.
SMART; SM00081; LRRCT; 1.
SMART; SM00086; LRRCT; 1.
SMART; SM00086; LRRCT; 1.
SMART; SM00086; LRRCTYP; 9.
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SEQUENCE
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EMBL; AK027262; BAB32403.1; -.
HSSP; P23945; 1XUN.
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InterPro; IPR003598; Ig_C2.
InterPro; IPR003600; Ig_Like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001611; LRR.
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LHELLRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESAFHSVGNLETLIL
                                LH-----GNRLOGVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLEFLRL
                                                                   SHWPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLYYLRFLNLSYNPIGTIEGSM
                                                                                                                  RSNRLKLIPLGVFTGLSNLTKLDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
                                                                                                                                                                              FQGLERLQSLHLYRCQLSSLPGNIFRGLVSLQYLYLQENSLLHLQDDLFADLANLSHLFL 186
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Search completed: April 4, 2003, 12:08:15 Job time: 40 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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  Score
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284
1 NPWACDCRARPLWAWFQRAR.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                  Length
DB
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CH10_LISMO
MT2_CANGA
NODI_RHILT
DB15_BOVIN
SRY_AKOAZ
RR16_LOTJA
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HMAA_AEDAE
YLQC_BACSU
                                                                                                                 VP52_BPAPS
KEB2_ECOLI
VG30_BPMD2
VNS1_IACAO
VHED_BPPHL
AES4_ALLMI
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VXIS_BPPH8
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POL_HV1J3
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P94701 salmonella
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                                                                            5 bovine papi
8 bacteriopha
2 equus cabal
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8 influenza a
1 bacteriopha
9 alligator m
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1 notophthalm
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aedes aegyp
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            bos taurus
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escherichia
      akodon
                    candida gla
rhizobium l
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				Ξ.	RESULT 1 MERT_STRL1
	ALIGNMENTS				
P12151 oryza sativ P10359 sinapis alb P83107 bos taurus O9hu55 pseudomonas P56702 rattus norv P01478 atrax robus P16806 bungarus fa P36866 lymantria d P15856 apis mellif O51639 borrelia bu	1 RR16_ORYSA 1 RR16_SINAL 1 BOP1_BOVIN 1 BXA2_SAMCY 1 GLRX_PSEAE 1 DB15_RAT 1 TXRO_ATRO 1 WX51_BUNFA 1 YPE1_NPVLD 1 HMAA_APIME 1 Y696_BORBU 1 YPE4_NPVLD	85 100 100 100 84 87 42 67 74 88	13.0 13.0 13.0 13.0 12.9 12.9 12.7 12.7 12.7	37 36.53 36.55 363 363 363	60000000000000000000000000000000000000

В ş Matches Query Match Best Local : MERT_STRLI STAN P30345; 01-APR-1993 (Rel. 2 01-APR-1993 (Rel. 2 01-NOV-1997 (Rel. 2 METAL METAL METAL METAL TRANSMEM TRANSMEM This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). SEQUENCE "Cloning and DNA sequence analysis of the mercury resistance genes Streptomyces lividans."; Mol. Gen. Genet. 236:76-85(1992). -I- FUNCTION: INVOLVED IN MERCURIC TRANSPORT. PASSES A HG(2+) ION FROM THE PERIPLASMIC MERP PROTEIN TO THE MERCURIC REDUCTASE Streptomyces lividans. Streptomyces lividans. Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. EMBL; X65467; CAA46463.1; PIR; S23611; S23611. PIR; S30171; S30171. STRAIN=66 / 1326; MEDLINE=93156687; PubMed=1494353; Sedlmeier R., Altenbuchner J.; -!- SUBCELLULAR LOCATION: Integral membrane protein. fransport; SEQUENCE FROM N.A. MERT. Mercuric transport protein 52 1 NPW----ACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDLRALRE SPWLLAPAAVLLAGALTWWLRRRRTGNGDACCLPAPRTDQHDRDLLRK 99 14; Similarity Mercury: 19 43 43 31 31 32 82 82 83 100 AA; Conservative STANDARD; . 25, Created) . 25, Last sequ . 35, Last anno Mercuric | 39 | 63 | 63 | 1 | 31 | 1 | 32 | 1 | 82 | 1 | 83 | 1 | 10353 MW; 18.7%; sequence update) annotation update) (Mercury ion transport protein). Score 53; DB Pred. No. 4.4; 4; Mismatches C resistance; Transmer POTENTIAL. POTENTIAL. HG(2+) (POTENTIAL). HG(2+) (POTENTIAL). HG(2+) (POTENTIAL). HG(2+) (POTENTIAL). HG(2+) (POTENTIAL). HG(2+) (POTENTIAL). 4; PRT; (POTENTIAL). (POTENTIAL). 100 DB 1; Length 100; 4.4; Transmembrane ⋧ 26; CRC64; Indels 4 Gaps of بر

RESULT

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MERP_SALTI
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Best Local :
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P94186;
01-NOV-1997
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15-JUN-2002 (Rel. 41, Last annotation update)
Mercuric transport protein periplasmic component precursor
(Periplasmic mercury ion binding protein) (Mercury scavenger protein).
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Plasmid Incl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transposons in environmental bac
Mol. Microbiol. 24:321-329(1997)
-!- FUNCTION: MERCURY SCAVENGER
                                                                                                                                                                                                                                                                                                                                Plasmid.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Intercontinental spread of promiscuous mercury-resistance transposons in environmental bacteria.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yurieva O., Kholodii G., Minakhin L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-97303088; PubMed-9159519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=512;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                   METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00946; HGSCAVENGER. PROSITE; PS01047; HMA_1; 1. PROSITE; PS50846; HMA_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y08993;
HSSP; P04129;
P94701; 008125; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Mercuric transport protein periplasmic component precursor (Periplasmic mercury ion binding protein) (Mercury scavenge)
                                                                MERP_SALTI
P94701; 008
                                                                                                                                                                                                                                                                              METAL
                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                       Transport; Mercuric resistance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001802; HG_scavenger.
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                                                                                                                                                                       11 PLWAWFORARVSSSDVTCATPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: MERCURY SCAVENGER THAT
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                                                                                                                                                                                                 Conservative
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36
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                                                                                                                                                                                                                                                                  HG(2+) (POTENTIAL).
HG(2+) (POTENTIAL).
                                                                                                                                                                                                                                                                                             HMA.
                                                                                                                                                                                                                             Score 47;
                                                                                                                                                                                                                                                      93988DE054D8AA7F CRC64;
                                                                                                                                                                                                                                                                                                           COMPONENT
                                                                                                                                                                                                                                                                                                                      POTENTIAL.
MERCURIC TRANSPORT
                                                                                                                                                                                                                Pred.
                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                            Periplasmic; Metal-binding; Signal;
                                                                                                                                                                                                     Mismatches
    protein) (Mercury scavenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AT SPECIFICALLY BINDS TO OF MERCURIC REDUCTASE (MERA)
                                                                                                                                                                                                                  No
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                                                                                                                                                                                                                              Length 91;
                                                                                                                                                                                                                                                                                                                         PROTEIN PERIPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kalyaeva
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ONE HG(2+)
A) VIA THE
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        protein)
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Query Match
Best Local S
                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterobacter agglomerans (Pantoea agglomerans), Enterobacter cloacae. Plasmid pHCM1, Plasmid pKLH272, and Plasmid pKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MERP OR HCM1.153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=S.typhi; STRAIN=CT18; PLASS MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=601, 549,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way nodified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yurieva O., Khologii w., .....
Mindlin S., Nikiforov V.;
"Intercontinental spread of promiscuous mercury-resistance
"Intercontinental spread of bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=E.agglomerans, and E.cloacae; STKALTSN:
PLASMID=PKLH272, and pKLH256; TRANSPOSON=TN5036;
MEDLINE=97303088; PubMed=9159519;
Yurieva O., Kholodii G., Minakhin L., Gorlenko Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transposons in environmental Mol. Microbiol. 24:321-329(19)
                                                                                                                                                                                        DOMAIN
METAL
                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00946; HGSCAVENGER PROSITE; PS01047; HMA_1; 1 PROSITE; PS50846; HMA_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y09025; CAA70
HSSP; P04129; 1AFJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL513383; CAD09748.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                          Plasmid; Complete proteome
                                                                                                                                                                                                                                                                                                                                     Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001802; HG_scavenger
                                                                                                                                                                    METAL
11 PLWAWFQRARVSSSDVTCATPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Periplasmic SIMILARITY: CONTAINS 1 HMA DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: MONOMER (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y08992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y08992; CAA70182.1;
Y09025; CAA70229.1;
                                                 Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001934; HeavyMe_transpt.
                                                                                                                                                                                                                                                                                                                                   Mercuric resistance; Periplasmic; Metal-binding; Signal;
                                                                                                                                                  91
                                                    Conservative
                                                                                                                                                                      \begin{smallmatrix}3&2\\3&3\\3&6\end{smallmatrix}
                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                    HMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CT18; PLASMID-PHCM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            550;
                                                                                                                                                  9611 MW;
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                                                                             16.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and E.cloacae; STRAIN=KH72,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gamma subdivision;
            32
                                                         4;
                                                                          Score 46; DE
Pred. No. 32;
                                                                                                                                                  HG(2+) (POTENTIAL).
HG(2+) (POTENTIAL).
E1298ECBCE2FBFD4 CRC64;
                                                                                                                                                                                                                                              POTENTIAL.
MERCURIC TRANSPORT
COMPONENT.
                                                                                                                                                                                                                          HMA
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                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MERCURIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIFICALLY BINDS TO ONE HG(2+)
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                                                              9;
                                                                                                        Length 91;
                                                                                                                                                                                                                                                                          PROTEIN
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                                                                Indels
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ACYO_CHICK
                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
YKK2_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                      01-FEB-1994
01-FEB-1994
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam: pF00708; Acylphosphatase; 1.
Prints; pr00112; Acylphosphatase; 1.
ProDom; PD001884; Acylphosphatase; 1.
ProSite; ps00150; Acylphosphatase; 1.
PROSITE; ps00151; ACYLPHOSPHATASE_2; 1.
PROSITE; ps00151; ACYLPHOSPHATASE_2; 1.
Hydrolase; Acetylation; Multigene family.
MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Muscle;
MEDLINE-88139274; Pubmed-2830254;
Ohba Y., Minowa O., Mizuno Y., Sh
                     SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                            YKK2_CA
P34279;
                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                           Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohba Y., Minowa O., Pitter.
"The primary structure of chicken
         Wilson
                                                                                                                 NCBI_TaxID=6239
                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A41513; QPCH2.
HSSP; P41500; 2ACY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Acylphosphate phosphohydrolase) (Isozyme CH2).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Acylphosphatase, organ-common type isozyme (EC 3.6.1.7)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIFFERENT TISSUES.
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: ITS PHYSIOLOGICAL ROLE IS NOT YET CLEAR.
CATALLYIC ACTIVITY: An acyl phosphate + H(2)0 = a fatty acid anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    + phosphate.
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                                                                                                                                                                                                                                                                                                                                                  CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001792; Acylphosphatase.
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    Ainscough
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                                                                                                                                                                                                                                                      (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                           (Rel. 28, Last sequence update) (Rel. 41, Last annotation updat protein C02F5.2 in chromosome
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                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                   28,
28,
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  Anderson K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45; DB
Pred. No. 46;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACYLPHOSPHATASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shiokawa
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osome III.
  Baynes
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                                                                                                                                                          Rhabditida;
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  Berks
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P12498;
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                                                                                                                                                          and P1' variable, but often Pro.
                                                                                                                                                                                                          AIDS Res.
                                                                                                                                                                                                                     MEDLINE-89352108; PubMed-2669897;
Komlyama N., Hattori N., Inoue J., Sakuma S., Kurimura "Nucleotide sequences of gag and env genes of a Japanes HIV-1 and their expression in bacteria.";
                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1989 (Rel. 12, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
POL polyprotein [Contains: Protease (Retropapsin)
Reverse transcriptase (EC 2.7.7.49); Ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M. Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
                                                                                                            -! - PTM:
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         Viruses; Retroid viruses;
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Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=11694;
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Hypothetical
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                                                               SIMILARITY: THE PROTEASE BELONGS KNOWN AS THE RETROPEPSIN FAMILY.
                                                                                                                               phosphomonoester.
CATALYTIC ACTIVITY: N deoxynucleoside triphosphate =
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   SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
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es; Retroviridae; Lentivirus.
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PROSITE; PS00175; ASP_PROT_EFFOV; 1.

PROSITE; PS50175; ASP_PROT_EFFOV; 1.

PROSITE; PS50175; ASP_PROT_EFFOV; 1.

Nuclease; Transferase; RNA-directed DNA polymerase.

CHAIN 57 >100

PROTEASE.

CHAIN 57 >100

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15-JUN-2002 (Rel. 41, Last annotation update)
Mercuric transport protein periplasmic component precursor
(Periplasmic mercury ion binding protein) (Mercury scavenger protein).
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                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Misra T.K., Brown N.L., Fritzinger D.C., Pridmore Haberstroh L., Silver S.; "Mercuric ion-resistance operons of plasmid R100 &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TRANSPOSON=Tn501;
MEDLINE=85014891;
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SIMILARITY: CONTAINS 1
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                    A03557; RGPSHA.; P04129; 1AFJ.
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IPR001969;
IPR001802; HG_scavenger
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Mercuric transport protein periplasmic component precursor
Mercuric mercury ion binding protein) (Mercury scavenger protein).
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Pfam; PF00403; HMA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transposable element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00946; HGSCAVENGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MERP_PSEFL
Q51770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transport; Mercuric resistance; Periplasmic; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of the pMER327/419, 330 and Gene 146:73-78(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid pMER327
                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94341572; Pu
Hobman J., Kholodii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas fluorescens
                                                                                                                                                                                                       EMBL; X73112; CAA51540.1;
HSSP; P04129; LAFJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=294;
    SIGNAL
                            Plasmid
                                                                         PROSITE; PS01047; HMA_1; PROSITE; PS50846; HMA_2;
                                                                                                                    PRINTS; PR00946; HGSCAVENGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      furieva O.;
                                               Transport;
                                                                    PROSITE;
                                                                                                                                                               InterPro;
                                                                                                                                                                                    InterPro; IPR001802; HG_scavenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Periplasmic (Probable).
SIMILARITY: CONTAINS 1 HMA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: MERCURY SCAVENGER THAT SPECIFICALLY BINDS TO ONE HG(2+) ION AND WHICH PASSES IT TO THE MERCURIC REDUCTASE (MERA) VIA THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MERT PROTEIN.
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                                                                                                                                            PF00403; HMA;
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8; Conserv
                                                                                                                                                                                                                                                                                                                                               non-profit institutions as long
                                                                                                                                                            IPR001934;
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                                                    Mercuric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pubMed=8063107;
ii G., Nikiforov V., Ritchie D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9491 MW;
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                                                 resistance; Periplasmic; Metal-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.8%;
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                                                                                                                                                                 HeavyMe_transpt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 1;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HG(2+) (POTENTIAL).
HG(2+) (POTENTIAL).
6D6DB86B5FCA20CE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSPORT
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36.48;

Pred. No. 1e+02;

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Best Local S
Matches 8
           Query Match
                                                                                                                                                                                      Plasmid.
SIGNAL
                                                     METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                       DOMAIN
                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                      InterPro; IPR001802; HG_scavenger.
InterPro; IPR001934; HeavyMe_transpt.
Pfam; PF00403; HMA; 1.
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M24940; AAA98223.1; -. PIR; C33858; C33858. HSSP; P04129; 1AFJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclfora G., Chu L., Silver S., Misra T.K.;

"Mercury operon regulation by the merR gene of the organomercurial resistance system of plasmid pDU1358.";

J. Bacteriol. 171:4241-4247(1989).

-I- FUNCTION: MERCURY SCAVENGER THAT SPECIFICALLY BINDS TO ONE HG(2+) ION AND WHICH PASSES IT TO THE MERCURIC REDUCTASE (MERA) VIA THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Mercuric transport protein periplasmic component precursor
(Periplasmic mercury ion binding protein) (Mercury scavenger protein).
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SEQUENCE
                                                                                                    METAL
                                                                                                                                                                                                                                                                                                 PRINTS; PRO0946; HGSCAVENGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serratia marcescens.
                                                                                                                                                                                                                                  ransport;
                                                                                                                                                                                                                                                  ROSITE; PS01047; HMA_1; ROSITE; PS50846; HMA_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-89327136; Pubmed-2666393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma
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nes 8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: Periplasmic (Probable).
SIMILARITY: CONTAINS 1 HMA DOMAIN.
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       Score
                                                                                                                HMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB
Pred. No. le+0
4; Mismatches
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                                              HG(2+) (POTENTIAL).
HG(2+) (POTENTIAL).
21EB0D79E9795069 CRC64;
                                                                                                                                         COMPONENT
                                                                                                                                                            POTENTIAL.
MERCURIC TRANSPORT
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HG(2+) (POTENTIAL).
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                                                                                                                                                                                                                             Periplasmic;
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       42;
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       DВ
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    1;
                                                                                                                                                                                                                      Metal-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
Length 91;
                                                                                                                                                            PROTEIN
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                                                                                                                                                       PERIPLASMIC
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for
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Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-BOULDE.

Misra T.K., Brown N.L., Fritzinger C.C.,

Misra T.K., Brown N.L., Fritzinger C.C.,

Misra T.K., Brown N.L., Fritzinger C.C.,

Haberstroh L., Silver S.;

"Mercuric ion-resistance operons of plasmid R100 @

"Mercuric ion-resistance operons including the common of the operon including the cand the first two structural genes."

and the first two structural genes."

Natl. Acad. Sci. U.S.A. 81:5975-5979(1984).
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P04129; P07042;
01-NOV-1986 (Rel. 03
01-NOV-1986 (Rel. 03
15-JUN-2002 (Rel. 41
Mercuric transport p
                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and the statement is not removed.
    EMBL; J01730;
                                         entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98313266; PubMed-9649312;
MEDLINE-9831266; PubMed-98493126; PubMed-9849326; PubMed-984956; PubMed-984956; PubMed-984956; PubMed-984956; PubMed-984956; PubMed-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steele R.A., Opella S.J.;
"Structures of the reduced and mercury-bound forms
"Structures of the reduced the bacterial mercury deto
                                                                                                                                                                                                                                                                                                                                                                     "NMR solution structure of the oxidized form binding protein involved in bacterial mercuri Biochemistry 37:9316-9322(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR. MEDLINE=97332449; Pubmed=9188683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry 36:6885-6895(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmid NR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-85159407; PubMed-6530603; Barrineau P., Gilbert P., Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-85014891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wisdom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid IncFII NR1
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Mercuric transport protein periplasmic component precursor
(Periplasmic mercury ion binding protein) (Mercury scavenger protein).
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                                                                                                                                                                                                                       SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: F
SIMILARITY: CONTAINS 1
                                                                                                                                                                                                                                                                                                                                                      FUNCTION: MERCURY
                                                                                                                                                                                                                                                                                                        MERT PROTEIN.
                                                                                                                                                                                                                                                                                                                 FUNCTION: MERCURY SCAVENGER THAT ION AND WHICH PASSES IT TO THE ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence
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AAA92262.1;
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                                                                                                                                                                                                                                                                                                                         MERCURIC
                                                                                                                                                                                                                                                                                                                                               SPECIFICALLY BINDS TO ONE HG(2+)
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                                                                                     and
                                                                                                                                                       EMBL
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                                                                                                                                                                        a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
HMAA_MANSE
Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; K03089; AAB59076.1; -.
PIR; AQ3556; RGEBHD.
PDB; 1AF1; 23-JUL-97.
PDB; 1AFJ; 23-JUL-97.
PDB; 2HQ1; 11-NOV-98.
InterPro; IPR001802; HG_scavenger.
InterPro; IPR001934; HeavyMe_transpt.
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METAL
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                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                         Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Endopteryota; Lepidoptera; Ginsecta; Pterygota; Neoptera; Endopteryota; Lepidoptera; Gitrysia; Sphingiodea; Sphingidae; Sphinginae; Manduca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HMAA_MANSE
                                                                                                                                                                                                                                            the lepidopteran, Manduca sexta.";

Development 112:119-129(1991).

-i- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART
-i- FUNCTIONAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
REQUIRED FOR SEGMENTAL IDENTITY OF THE FIRST THROUGH TENTH
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLLNE=92120089; PubMed=1685112;

Magy L.M., Booker R., Riddiford L.M.;

"Isolation and embryonic expression of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [ransposable element;
                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                          EMBL; S77989; AAB21131.2; ALT_SEQ HSSP; P02833; 9ANT.
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7130;
                         InterPro; IPR00047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 PVWAATQTVTLAVPGMTCAACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 PLWAWFQRARVSSSDVTCATPP
                                                                                                                                                                                                      SUBCELLULAR LOCATION: Nuclear (Probable). SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                     ABDOMINAL SEGMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR00946;
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8; Conserv
               IPR001356;
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nilarity 36.4%;
Conservative
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91
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33
51
                Homeobox.
                                HTH_repressr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid; 3D-structure
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HG(2+) (POTENTIAL).
S -> T (IN REF. 2).
822183AC323031A5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97
                                                                                                      (See http://www.isb-sib.ch/announce/
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Best Local 9
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Best Local Similarity
Matches 12; Conserv
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Q9T1P6;
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PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00027; HOMEOBOX_1; 1.

PROSITE; PS50071; HOMEOBOX_2; 1.

Homeobox; DNA-binding; Developmental protein; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=99420383; PubMed=10489345;

van der Wilk F., Dullemans A.M., Verbeek M., van den Heuvel J.F.J.M.;

van der Wilk F., Dullemans A.M., Verbeek M., van den Heuvel J.F.J.M.;

rIsolation and characterization of APSE-1, a bacteriophage infecting the secondary endosymbiont of acyrthosiphon pisum.";

Virology 262:104-113(1999).
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
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                     P13965;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
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SEQUENCE FROM N.A.
MEDLINE-98300335; PubMed-9636706;
Ford M.E., Sarkis G.J., Belanger A.E., !
Ford M.E., Sarkis G.J., Belanger A.E., !
This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
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15-DEC-1998
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Viruses, dsDNA viruses, no
unclassified Siphoviridae.
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11; Conserv
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9 28 H-T-H MOTIF (BY SIMILARITY).
71 AA: 7605 MW: BDD9D998ABDAE04C CRC64;
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Pfam; PF00600; Flu_NS1; 1.
ProDom; PD000613; Flu_NS1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Camels in Mongolia.";
Virology 197:558-563(1993).
-I- ALTERNATIVE PRODUCTS: NS1 AND NS2 PROTEINS ARE PRODUCED ALTERNATIVE SPLICING OF SEGMENT 8.
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P26148;
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NCE 88 AA; 10391 MW; 52071A2E678E5BCE CRC64;
                                                                                                                                                                               Similarity 34.9
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
17; Conser
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Rel. 22, Last sequence up
Rel. 40, Last annotation
Rel. 40, Last annotation
Rel. 40, Fragment).
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10396 MW;
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34.5%;
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Pred. No. 1
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Pred. No. 1.8e
7; Mismatches
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2003,

08:25:23

7, .

	GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
OM protein - pro	OM protein - protein search, using sw model
Run on:	April 4, 2003, 08:21:41 ; Search time 18.8889 Seconds (without alignments) 254.473 Million cell updates/sec
Title: Perfect score:	US-09-972-546-2_COPY_261_310 284
	1 NPWACDCRARPLWAWFQRARPPERQGRDLRALREADFQAC 50
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	283224 segs, 96134422 residues
l number of	L number of hits satisfying chosen parameters: 28758

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seg length: 40 Maximum DB seg length: 100

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result	Score	Query	Length	B	ID	Description
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o 00	. 4	ij	85	N	S44604	
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			hypothetical prote	_	8	sox protein - less	7 P	210		hypothetical prote	transcription fact	3	hypothetical prote	Sry-related sequen	hypothetical prote

ALIGNMENTS

Qy 2 PWACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDLRALR 43	Query Match 20.1%; Score 57; DB 2; Length 100; Best Local Similarity 29.2%; Pred. No. 5.2; Matches 14; Conservative 6; Mismatches 22; Indels 6; Gaps 1;	A; Introns: 15/1; 72/2 A; Introns: 15/1; 72/2 C; Superfamily: mouse adenovirus early E3 protein	A;Molecule type: DNA A;Residues: 1-100 <bea> A;Cross-references: GB:M33995; NID:g209915; PIDN:AAA42494.1; PID:g209917</bea>	A;Title: Transcription mapping of mouse adenovirus type 1 early region 3. A;Reference number: A46308; MUID:90177241; PMID:2137954 A;Accession: A46308	R;Beard, C.W.; Ball, A.O.; Wooley, E.H.; Spindler, K.R. Virology 175, 81-90, 1990	E3 class 1 protein - mouse adenovirus 1 C;Species: Mastadenovirus mus1 (mouse adenovirus 1) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999 C;Accession: A46308	RESULT 1 A46308
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S30171

mercuric ion transport protein merT - Streptomyces lividans
(;Species: Streptomyces lividans
(;Species: Streptomyces lividans
(;Date: 30)-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Oct-1999
(;Accession: \$30171; \$23611
R;Sedlmeier, R.; Altenbuchner, J.
Mol. Gen. Genet. 316, 76-85, 1992
A;Title: Cloning and DNA sequence analysis of the mercury resistance genes of Strepto
A;Reference number: \$30168; MUID:93156687; PMID:1494353
A;Accession: \$3017.

A; Molecule type: DNA
A; Residues: 1-100 <ALTY
A; Cross-references: EMBL: x65467; NID: g47180; PIDN: CAAA6463.1; PID: g47184
A; Experimental source: Strain 1326
C; Genetics:
A; Gene: merT
C; Function:
A; Description: involved in transport of mercury ions from periplasm into cytoplasm; p
A; Pathway: mercury resistance
A; Note: mercury resistance operon
C; Keywords: binding protein-dependent transport system; mercury transport; transmembrane #status predicted <TM1>
F; 15-31/Domain: transmembrane #status predicted <TM3>
F; 55-71/Domain: transmembrane #status predicted <TM3>

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RESULT
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A;Molecule type: DNA
A;Residues: 1-67 <SEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-May-2000 C;Accession: T30718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein 116R - Molluscum contagiosum virus
N;Alternate names: MC116R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            agrobacterium virulence homologue virB7 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
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                                                                                                                                                                                                                                                                                                                                                                     R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references:
                                                                                                                                                        C; Genetics:
A; Gene: avhB7
                                                                                                                                                                                            A; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-88 <KUR>
                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: AD3180
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                                                                                                                                           A; Genome:
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                                                                      Matches
                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                    tle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens :ference number: AB2577; PMID:11743193
                                                                                                                                                                                                                                                                                                                                     thors: Yoo, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 SPWLLAPAAVLLAGALTWWLRRRTGNGDACCLPAPRTDQHDRDLLRK 99
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mes 15; Conserv
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   37
                                 10 RPLWAW-----FORARVSSSDVTCATPPERQGRDLRALREAD
                                                                                       Local Similarity
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                                                                                                                                         plasmid
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RPMWDWEGGSKLQQQQSNTSSSTSLTPFVKEASETSAFAHLD
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                                                                        Conservative
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29.2%;
                                                                                                                                                                                                                                                                                                                                                        Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.8%;
41.7%;
                                                                                       17.4%; 26.2%;
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Pred. No. 23;
4; Mismatches
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                                                                                     Score 49.5;
Pred. No. 39;
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McClel
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RESULT JE0210

орси2

acylphosphatase (EC 3.6.1.7) Ch2, skeletal muscle N; Alternate names: acylphosphate phosphohydrolase

chicken

Qy

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proteinase (EC 3.4.-.-) serine-like, NES1 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 07-May-1999 C;Accession: JE0210 R;Luo, L.; Herbrick, J.A.; Scherer, S.W.; Beatty, B.; Squire. J.: Diamandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Luo, L.; Herbrick, J.A.; Scherer, S.W.; Beatty, B.; Squire, J.; Diamandis, E.P. Biochem. Biophys. Res. Commun. 247, 580-586, 1998
A;Title: Structure characterization and mapping of the normal epithelial cell-specifi A;Reference number: JEO210; MUID:98321170; PMID:9647736
A;Accession: JEO210
                                                                                                                                                                                                                                                                                                               A;Experimental source: strain 9aSc
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Franca, D.J.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La J.D.; Junqueira, M.A.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, C.A.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Silva, R.G.; Santelli, R.V.; Sawa Rodrigues, V.; Rosa, A.G. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L. A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 19q13.3-13.4
C; Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-90 <LUO>
A;Cross-references: GB:AF055481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein XF1421 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: B82685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: GDB: PRSSL1; NES1
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A; Residues: 1-62 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: The genome sequence of the plant pathogen Xylella fastidiosa. A; Reference number: A82515; MUID:20365717; PMID:10910347 A; Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE003972; GB:AE003849; NID:g9106418; PIDN:AAF84230.1;
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Nature 406, 151-157, 2000
                                                                                                                                                                                                                                        A;Gene:
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Best Local
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                                                                                                                     Matches
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                                                    10 RPL-WAWFQRARVSSSDVTCATP---PERQGRDLRALREADFQA 49
                                                                                                                                              Local Similarity
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                                                                                                                                                    Score 45;
Pred. No.
                                                                                                                            Mismatches
                                                                                                                                                       1e+02;
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acetohydroxy acid synthase II, small chain [imported] - Salmonella enterica subsp. C:Species: Salmonella enterica subsp. enterica serovar Typhi A:Note: this species has also been called Salmonella typhi C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C:Accession: AE0924
                                                                                                                                                                 th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dow
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A:Tittle: Complete genome sequence of a multiple drug resistant
A:Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 0:
C;Accession: A41513
R;Ohba, Y; Minowa, O; Mizuno, Y; Shiokawa, H.
J. Blochem, 102, 1221-1229, 1987
A;Title: The primary structure of chicken muscle acylphosphatase A;Accession: A41513; MUID:88139274; PMID:2830254
A;Accession: A41513
                                                                                                     A; Molecule type: DNA
A; Residues: 1-86 < PAR>
                                                                                                                                                                                                                                                                            R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N
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                                                                                      A; Cross-references:
                                                                                                                                           A; Status: preliminary
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A; Residues: 1-85 < AND>
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A;Description: Sequence of the C. elegans cosmid CO2F5
A;Reference number: S44603
A;Accession: S44604
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                         AE0924
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      Query Match
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Best Local (
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Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Aug-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 SSSDVTCATPPERQGRDLRALREADFQA 49
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12; Conserv
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9; Conser
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                                                                                 GB:AL513382;
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  15.18;
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26.1%;
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                                                                           PIDN:CAD09415.1;
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Pred. No.
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Pred. No. 1.6e
9; Mismatches
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<u>3</u>;
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1.8e+02;
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2
                                                                           PID:g16504533; GSPDB:GN00176
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98
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A; Molecule type: DNA
A; Residues: 1-79 <STO>
A; Cross-references: GB:
C; Genetics:
A; Gene: CC2450
acetolactate synthase (EC 4.1.3.18) isozyme II small chain [imported] - YC:Species: Yersinia pestis
C:Species: Versinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C:Accession: AB0475
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, I., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre
                                                                                                                                                     AB0475
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein CC2450 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Decies: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: A87553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
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C;Species: Saccharomyces cerevisiae
C;Date: 15-Jan-1999 #sequence_revision 15-Jan-1999 #text_change
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A; Residues: 1-65 <GRI>
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A; Accession: $78743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: S78743
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Best Local
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7; Conser
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Pred. No.
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Pred. No. 2.5e
4; Mismatches
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2.5e+02;
3;
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3e+02;
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                                                                                                                                                                                                                                                                                                                                  Length 79
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..; Haft, D.H.; Ko
.. J.C.; Fraser, C
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A; Reference number: AF
A; Accession: AB0475
A; Status: preliminary
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A;Genome: plasmid
C;Superfamily: mercuric resistance operon re
C;Keywords: mercury transport; metal binding
F;1-19/Domain: signal sequence #status predi
F;20-91/Product: mercuric resistance operon
F;28-57/Domain: heavy-metal-associated homol
F;33,36/Binding site: mercury (Cys) #status
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A; Residues: 1-85 < KUR>
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                                                                                                                                                                                                                                                                                                                                                 mercuric resistance operon regulatory protein precursor - plasmid to; Alternate names: mercuric-ion-binding protein; mercury scavenger C; Species: plasmid NR1 C; Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 16-C; Accession: S09524
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proc. Natl. Acad. Sci. U.S.A. 81, 5975-5979, 1984
A;Title: Mercuric ion-resistance operons of plasmid R100
A;Reference number: A03556; MUID:85014891; PMID:6091128
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A; Residues: 1-91 <MIS>
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A; Genome: proceed to C; Superfamily:
                                                                                                                                                                                                                                                                                          R;Barrineau, P.; Gilbert, P.; Jackson, W.J.; Jones, C.S.;
J. Mol. Appl. Genet. 2, 601-619, 1984
                                                                                                                  A;Cross-references: EMBL:K03089; NID:g150389;
                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-91 <BAR>
                                                                                                                                                                                                                                  J. Mol. Appl. Genet. 2, 601-619, 1984
A; Title: The DNA sequence of the mercury resistance operon
A; Reference number: $07447; MUID:85159407; PMID:6530603
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No. 3.2e+02;
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C;Keywords: mercury transport; metal binding; periplasmic space F;1-19/Domain: signal sequence #status predicted <SIG>F;20-91/Product: mercuric resistance operon regulatory protein #F;28-57/Domain: heavy-metal-associated homology <HMA>F;33,36/Binding site: mercury (Cys) #status predicted
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N;Alternate names: mercuric-ion-binding protein; mercury scavenger protein
C;Species: Pseudomonas aeruginosa
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A; Residues: 1-91 <MIS>
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10: /cgn2_6/ptcodata/2/pubpaa/USO9_NEW_PUB.pep:*

11: /cgn2_6/ptcodata/2/pubpaa/USO9_NEW_PUB.pep:*

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US-09-978-697-400
US-09-978-192A-400
US-09-998-33A-400
US-09-998-189-400
US-10-121-049-382
US-10-121-049-382
US-10-175-746-382
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APPLICANT: Napier, Mary A.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;

APPLICANT: Pan, James;

APPLICANT: Pan, James;

APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2630PLC1

CURRENT APPLICATION NUMBER: US/09/978,295A

CURRENT FILING DATE: 2001-01-15

PRIOR APPLICATION NUMBER: 60/062250

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17
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US-09-78-295A-400
; Sequence 400, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                               Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James:
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Grimaldi, J. Christopher
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NUMBER: 60/064249
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PRIOR

APPLICATION NUMBER: FILING DATE: 1998-0: APPLICATION NUMBER:

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1998-03-11

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FILING DATE: 1998-03-10 APPLICATION NUMBER: 60/0 FILING DATE: 1998-03-11

60/077632

APPLICATION NUMBER: 60/077450

1997-11-

60/066364 60/065311

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APPLICATION NUMBER: FILING DATE: 1998-0

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OR APPLICATION NUMBER: 60/078910
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078939
OR FILING DATE: 1998-03-20
OR FILING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079294
OR FILING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079656
OR FILING DATE: 1998-03-26
OR APPLICATION NUMBER: 60/079664
OR APPLICATION NUMBER: 60/079664
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PRIOR PRIOR

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NUMBER: 60/ : 1998-03-27

60/079689

APPLICATION NUMBER: 60/079663 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079728 FILING DATE: 1998-03-27

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R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/079786
R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/079920
R FILING DATE: 1998-03-30
R APPLICATION NUMBER: 60/079923

NUMBER: 60/079920 1998-03-30

NUMBER: 60/079786 1998-03-27

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60/080327 60/080194 60/080165 60/080107 60/080105

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NUMBER: 60/081071

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NUMBER: NUMBER:

60/081049 60/081070

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60/081203

NUMBER: 60/1: 1998-04-09

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NUMBER: 60/081195: 1998-04-08

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NUMBER: 60/ : 1998-04-01 NUMBER: 60/080333 : 1998-04-01 NUMBER: 60/080328 NUMBER: 60/ : 1998-04-01 NUMBER:

60/080334

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RESULT 2
US-09-978-697-400
                                                                                                                                                                                            APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napole
                                                                                                                                                                                                                                                                                                                     GENERAL
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FILING DATE: 1998-05-1
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Gao, Wel-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                       Filvaroff, Ellen
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Desnoyers, Luc
                                                                                                                                                                                                                                                                          Baker Kevin P.
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065364
PRIOR APPLICATION NUMBER: 60/066364
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/0:
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/0:
PRIOR FILING DATE: 1998-03-13
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/0
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PRIOR FILING DATE: 1998-03-11
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CURRENT FILING DATE: 2001-10-16
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OR FILING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079656
OR FILING DATE: 1998-03-26
OR APPLICATION NUMBER: 60/079664
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079689
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079663
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079663
OR FILING DATE: 1998-03-27
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OR APPLICATION NUMBER: 60/079920

OR FILING DATE: 1998-03-30

OR APPLICATION NUMBER: 60/079923

OR FILING DATE: 1998-03-30

OR APPLICATION NUMBER: 60/080105

OR APPLICATION NUMBER: 60/080105

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                                                         APPLICATION NUMBER: 60/080107
FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080165
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60,078939
FILING DATE: 1998-03-20
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                        APPLICATION NUMBER:
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FILING DATE: 1998-03-20
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Wood, William I.
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APPLICATION NUMBER: 60/081955 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081817

NUMBER: 60/081817 1998-04-15

FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-15

60/081819

APPLICATION NUMBER:

60/081952

PRIOR PRIOR

R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/06
R APPLICATION NUMBER: 60/06
R APPLICATION NUMBER: 60/06
PR FILING DATE: 1998-04-09

60/081229 60/081203

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DR FILING DATE: 1998-04-08
DR APPLICATION NUMBER: 60/081049
DR FILING DATE: 1998-04-08
DR APPLICATION NUMBER: 60/081071
DR FILING DATE: 1998-04-08
DR APPLICATION NUMBER: 60/081195
DR APPLICATION NUMBER: 60/081195

APPLICATION NUMBER: 60/081070

1998-04-01

FILING DATE:

OR FILING DATE: 1998-04-01

OR APPLICATION NUMBER: 60/080328

OR FILING DATE: 1998-04-01

OR APPLICATION NUMBER: 60/080333

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OR APPLICATION NUMBER: 60/080334

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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/
FILING DATE: 1998-05-13
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FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085582
FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085339
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FILING DATE: 1998-05-15
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FILING DATE: 1998-05-15
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                                                                                                                                                                   YLRLNDNPWVCDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCAVAT
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Similarity 42.2%;
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1998-05-07
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                                                         PLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRL
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Pred. No. 1.1e-57;
8; Mismatches 140
                                                                                                                                             -PPAA-----
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APPLICATION NUMBER: 60/083392 FILING DATE: 1998-04-29

APPLICATION NUMBER: 60/083495

FILING DATE: 1998-04
APPLICATION NUMBER:
FILING DATE: 1998-04

1998-04-28

60/083322

APPLICATION NUMBER: 60/0 FILING DATE: 1998-04-23

60/082796

APPLICATION NUMBER: 60/082700 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082797 FILING DATE: 1998-04-22

FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082704
FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082804
FILING DATE: 1998-04-22

APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-21 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081838 FILING DATE: 1998-04-15

APPLICATION NUMBER: 60/082569

OR FILING DATE: 1998-04-29
OR RILING DATE: 1998-04-29
OR REPLICATION NUMBER: 60/083496
OR APPLICATION NUMBER: 60/083499
OR APPLICATION NUMBER: 60/083545
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083554
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APPLICATION NUMBER: FILING DATE: 1998-04

60/083742 60/084366 60/084414

APPLICATION NUMBER: 60/083500 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083559 FILING DATE: 1998-04-29

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RESULT 3
US-09-978-192A-400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/62250
PRIOR FILING DATE: 1997-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C9
FILE REFERENCE: P2630P1C9
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APPLICANT:
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CURRENT FILING DATE: 2001-10-15
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APPLICANT: Baker Kevin P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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RETLING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/06
OR FILING DATE: 1997-11-21
OR APPLICATION NUMBER: 60/07
OR FILING DATE: 1998-03-10
OR APPLICATION NUMBER: 60/07
OR FILING DATE: 1998-03-11
OR FILING DATE: 1998-03-11
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OR FILING DATE: 1998-03-11
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Williams, P. Mickey
Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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Goddard, Audrey
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Botstein, David
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APPLICANT: Baker Kevin P.
                                                                                                                                                                                                                                                APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PlC63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
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              DR APPLICATION NUMBER: 60/066364
DR FILING DATE: 1997-11-21
PR APPLICATION NUMBER: 60/077450
DR FILING DATE: 1998-03-10
DR APPLICATION NUMBER: 60/077632
DR FILING DATE: 1998-03-11
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Gao, Wei-Qiang
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Shelton, David L.
Stewart, Timothy A.
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Kuo, Sophia S.
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DR FILING DATE: 1998-03-11
DR APPLICATION NUMBER: 60/077649
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DR APPLICATION NUMBER: 60/077791
DR FILING DATE: 1998-03-12
DR APPLICATION NUMBER: 60/078004
DR FILING DATE: 1998-03-13
DR APPLICATION NUMBER: 60/078886
DR FILING DATE: 1998-03-20
DR APPLICATION NUMBER: 60/078936
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DR APPLICATION NUMBER: 60/078910
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Matches 191
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PRIOR APPLICATION NUMBER: 60/085704
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     Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                     Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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o. US20030004102A1
  Williams,
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                                                                                                             Kuo,
                                                                                                                        Kljavin,
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Gerritsen, Mary E.
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                                                                                                        avin, Ivar J.
Sophia S.
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                                                                                           Mary A.
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  P. Mickey
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Pred. No. 1.1e-57;
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CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/064311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
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PRIOR FILING DATE: 1998-03-11
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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APPLICATION NUMBER: 60/080107
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FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/079656
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APPLICATION NUMBER: 60/080333
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080334
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NUMBER: 60/081049
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OF FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084639
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                                                           APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maur
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FOR APPLICATION NUMBER: 60/085573
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OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084643
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/085339
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085338
OR FILING DATE: 1998-05-13
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APPLICATION NUMBER: 60/085689
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APPLICATION NUMBER: 60/085579
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FILING DATE: 1998-05-13
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191; Conservative
Beresini, Maureen
DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
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38;

Mismatches 140;

84;

Gaps

12;

Length 473; Indels

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APPLICANT: APPLICANT: APPLICANT:

Gao, Wei-Qiang Gerritsen, Mary

(1)

APPLICANT:

APPLICANT: APPLICANT:

Watanabe,Colin K Wood,William

Tumas,Daniel

ITLE OF INVENTION:

Zhang

APPLICANT:

APPLICANT: APPLICANT:

Sherwood, Steven Smith, Victoria Stewart, Timothy

Goddard, Audrey Godowski, Paul J. Gurney, Austin L.

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PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-08-26

APPLICATION NUMBER: 60 FILING DATE: 1997-09-1

60/059115 9-17 60/059117

FILING DATE: APPLICATION NUMBER:

1997-09-17

APPLICATION NUMBER:

APPLICATION NUMBER: 60/059113 FILING DATE: 1997-09-17

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OR APPLICATION NUMBER: 60/081203
OR APPLICATION NUMBER: 60/081203
OR FILING DATE: 1998-04-09
OR APPLICATION NUMBER: 60/081229
OR FILING DATE: 1998-04-09
OR FILING DATE: 1998-04-09
OR APPLICATION NUMBER: 60/081695
OR APPLICATION NUMBER: 60/081817
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OR FILING DATE: 1998-04-15
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R FILING DATE: 1997-12-11
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PR APPLICATION NUMBER: 60/083322
PR FILING DATE: 1998-04-28
PR APPLICATION NUMBER: 60/083545
PR FILING DATE: 1998-04-29
PR APPLICATION NUMBER: 60/084600
PR FILING DATE: 1998-05-07
PR FILING DATE: 1998-05-07
PR APPLICATION NUMBER: 60/084627
PR APPLICATION NUMBER: 60/084627
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R APPLICATION NUMBER: 1998-03
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                                                                                    DR APPLICATION NUMBER: 60/01
DR FILLING DATE: 1998-05-07
DR APPLICATION NUMBER: 60/01
DR FILLING DATE: 1998-05-12
DR APPLICATION NUMBER: 60/01
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FILING DATE: 1997-11-24
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APPLICATION NUMBER: 60/
FILING DATE: 1997-11-07
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FILING DATE: 1998-02-09
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/079663
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                                 FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/0
FILING DATE: 1998-05-13
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NUMBER: 60/085339
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1998-04-15
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FILING DATE: 1997-09-10
APPLICATION NUMBER: 60/059352
APPLICATION 1997-09-19
TO THE DATE: 1997-09-19
TO THE DATE: 1997-09-19

APPLICATION NUMBER: 60/059588 FILING DATE: 1997-09-19

FILING DATE: 1997-09
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FILING DATE: 1997-10-2*
APPLICATION NUMBER: 60/063327
APPLICATION 1997-10-27
APPLICATION NUMBER: 60/063327

APPLICATION NUMBER: 60/063127

FILING DATE: 1997-10-27
APPLICATION NUMBER: 60/063329
FILING DATE: 1997-10-27
APPLICATION NUMBER: 60/063550

APPLICATION NUMBER: 60/063561 FILING DATE: 1997-10-28

APPLICATION NUMBER:

60/063704

FILING DATE:

1997-10-28

FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/063045
FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/063082'
FILING DATE: 1997-10-31

APPLICATION NUMBER: 60/062814
FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/062816
FILING DATE: 1997-10-24

FILING DATE: 1997-10-17 APPLICATION NUMBER: 60/ FILING DATE: 1997-10-17

60/062287

APPLICATION NUMBER: 60/062285 FILING DATE: 1997-10-17 APPLICATION NUMBER: 60/062250 FILING DATE: 1997-10-17 APPLICATION NUMBER: 60/059836 FILING DATE: 1997-09-24

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FILING DATE: 1997-10 2-APPLICATION NUMBER: 60/C APPLICATION NUMBER: 60/C

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APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/
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FILING DATE: 19/98-06-11
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FILING DATE: 1998-06-04
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FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/086430
FILING DATE: 1998-05-22
                            YLRLNDNPWVCDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCAVAT 313
                                                   FLRLNANPWACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDLRALREADFQAC----
                                                                                           PERAFRGLHSLDRLLLHQNRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAPLRALQ
                                                                                                              TEHVERGLGSLDRLLLHGNRLQGVHRAAFRGLSRLTILLYLFNNSLASLPGEALADLPSLE 254
                                                                                                                                                                                                                        VLWLQAWQVAAP-CPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRIFLHGNRISHVP 73
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---PPAA-----PTRPGSRAR---
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-GNS 326
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Best Local Similarity 42.2
                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEO ID NOS: 550
SEO ID NO 382
LENGTH: 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C17
                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 47
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GPYHPIWTGRATDEEPLGLPKCCQPDAADKASVLEPGRPASAGNALKGRVPPGDSPPGNG
                                                                         FLRLNANPWACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDLRALREADFQAC----
                                                                                                            TLHLDRCGLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHGNRISSV
                                                     YLRLNDNPWVCDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCAVAT
                                                                                                                                 TEHVFRGLGSLDRLLLHGNRLQGVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLE
                                                                                                                                                                                                                           AASFRACRNLTILWLHSNVLARIDAAAFTGLALLEQLDLSDNAQLRSVDPATFHGLGRLH
                                                                                                                                                                                                                                          PGTFGS--NLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFQGLERLQ 134
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stewart, Timothy A. Tumas, Daniel
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5. US20030022239A1
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                             --PPAA-----PTRPGSRAR---
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Pred. No. 1.1e-57;
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RESULT 8
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 382
LENGTH: 473
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Best Local
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ORGANISM: Homo Sapien
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                                                                 YLRLNDNPWVCDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCAVAT 313
                                                                                                                                   PERAFRGLHSLDRLLLHQNRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAPLRALQ
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Godowski, Paul J.
Gurney, Austin L.
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les 191; Conservative 38
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SS-NHL----YGVAEAGAPPADPSTLYR-----DLPAEDSRGRQG--
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o. US20030027270A1
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ilarity 42.2%;
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Pred. No. 1.1e-57;
38; Mismatches 140;
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US-10-176-918-382
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LENGTH: 473
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Best Local
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APPLICANT:
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CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File W.
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Gurney, Austin L.
Sherwood, Steven
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o. US20030027275A1
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C382
                                                                                                                                                                         74 AASFRACRNITILWIHSNVIARIDAAAFTGIALIEQIDISDNAQIRSVDPATFHGIGRIH
                                                                                                                                                                                                                                                                                      TEHVFRGLGSLDRLLLHGNRLQGVHRAAFRGLSRLTILYLFNNSLASLFGEALADLPSLE
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                                            SS-NHL----YGVAEAGAPPADPSTLYR------DLPAEDSRGRQG-------
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                                                                                     GPYHPIWTGRATDEEPLGLPKCCQPDAADKASVLEPGRPASAGNALKGRVPPGDSPPGNG
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42.2%; Pred. No. 1.1e-57;
Live 38; Mismatches 140
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US-10-176-921-382
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LENGTH: 473
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GENERAL INFORMATION
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Best Local :
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CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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SGPRHINDSPFGTLPGSAEP--PLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRL 431
                                SS-NHL----YGVAEAGAPPADPSTLYR-----DLPAEDSRGRQG-----
                                                                   GPYHPIWTGRATDEEPLGLPKCCQPDAADKASVLEPGRPASAGNALKGRVPPGDSPPGNG
                                                                                                                                        YLRINDNPWVCDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCAVAT 313
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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Desnoyers, Luc
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b. US20030027276A1
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RESULT 13
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PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
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PRIOR FILING DATE: 2002-04-09
PRIOR PRICTON NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
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CURRENT FILING DATE: 2002-08-26
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PRIOR APPLICATION NUMBER: 60/085323
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APPLICATION NUMBER: 60/079728
                  APPLICATION NUMBER: 60/090691 FILING DATE: 1998-06-25
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Grimaldi, J. Christopher
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PR APPLICATION NUMBER: 60/151733

DR FILING DATE: 1999-08-31

DR APPLICATION NUMBER: 60/16418

DR FILING DATE: 1999-11-09

DR APPLICATION NUMBER: 60/166361

DR FILING DATE: 1999-11-16
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OR FILING DATE: 1999-04-26
OR APPLICATION NUMBER: 60/131270
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APPLICATION NUMBER: 60/169495
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APPLICATION NUMBER: 60/169835
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APPLICATION NUMBER: 60/
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FILING DATE: 1999-08-17
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AASFRACRNLTILWLHSNVLARIDAAAFTGLALLEQLDLSDNAQLRSVDPATFHGLGRLH
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APPLICATION NUMBER: 60/1
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FILING DATE: 1998-12-23
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                                                                                                                                               Score 808; DB 9;
Pred. No. 1.1e-57;
38; Mismatches 140;
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DR APPLICATION NUMBER: 60/099811

R FILING DATE: 1998-09-10

DR APPLICATION NUMBER: 60/099812

DR FILING DATE: 1998-09-10

DR APPLICATION NUMBER: 60/099816

DR FILING DATE: 1998-09-10

NR APPLICATION NUMBER: 60/09
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60/096791 3-17 60/096146

60/097986 60/098544

FILING DATE: 1998-08-10

60/095916

APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE:

1998-08-04 -80-866

60/095318

FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/095302
FILING DATE: 1998-08-04

DR FILING DATE: 1998-10-30
PAPPLICATION NUMBER: 60/106905
DR FILING DATE: 1998-11-03
PR APPLICATION NUMBER: 60/108787
OR FILING DATE: 1998-11-17
DR APPLICATION NUMBER: 60/10801
DR FILING DATE: 1998-11-17
DR APPLICATION NUMBER: 60/108049
DR FILING DATE: 1998-11-18
DR APPLICATION NUMBER: 60/112422
DR FILING DATE: 1998-12-15
DR APPLICATION NUMBER: 60/112422
DR FILING DATE: 1998-12-15
DR APPLICATION NUMBER: 60/112422

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Gaps 76 73

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APPLICATION NUMBER: 60/113296 FILING DATE: 1998-12-22 APPLICATION NUMBER: 60/113605

OR APPLICATION NUMBER: 60/10
R FILING DATE: 1998-09-25
DR APPLICATION NUMBER: 60/10
OR FILING DATE: 1998-09-24
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OR APPLICATION NUMBER: 60/10
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DR APPLICATION NUMBER: 60/10

60/106178 60/101922 60/101916

98/101/86 60/101741 60/101738 60/101477 60/100919 9-17 60/100848

60/106464 60/106248 APPLICATION NUMBER: 60/ FILING DATE: 1998-09-24 APPLICATION NUMBER: 60/ FILING DATE: 1998-09-24

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US-10-137-865-382
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                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper NUMBER OF SEO ID NOS: 550
SEO ID NO 382
SEO ID NO 382
                                                                                                                                Query Match
                                                                                                        Matches
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TYPE: PRT
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                                                                                                        Local Similarity 42.2
nes 191; Conservative
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                                                 PGTFGS--NLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFQGLERLQ 134
                                                                                                                                                                                                                                                                                                                                                                                                    Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Desnoyers, Luc
Filvaroff, Ellen
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Wood,William
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Gerritsen, Mary E
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                                                                                                                                                                                                                                                                                                                                                                                       Smith, Victoria
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                                                                                                                        36.3%;
42.2%;
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                                                                                                          Score 808; DB 9; 1
Pred. No. 1.1e-57;
8; Mismatches 140;
                                                                                                                                      Length 473;
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publication No. US20030032156A1
                                                                                                                                                                                                                                                              SEQ ID NO 382
LENGTH: 473
                                                                                                                                                         Matches
                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C162
CURRENT APPLICATION NUMBER: US/10/140,474
CURRENT FILING DATE: 2002-05-06
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 GDAPTEDDYWGGYGGEDQRGEQMCPGAACQAPP 394
                                                                                                                       18 LLMLLALPLAAPSCPMLCTCYSSPP-TVSCQANNESSVPLSLPPSTQRLFLQNNLIRTLR 76
                                                                                         15 VLWLQAWQVAAP-CPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRIFLHGNRISHVP 73
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SLHLYRCQLSSLPGNIFRGLVSLQYLYLQENSLLHLQDDLFADLANLSHLFLHGNRLRLL 194
                               AASFRACRNITTIWIHSNVLARIDAAAFTGLALLEQIDISDNAQIRSVDPATFHGLGRIH 133
                                               PGTFGS--NLLTLWLFSNNLSTIYPGTFRHLOALEELDLGDNRHLRSLEPDTFQGLERLQ 134
                                                                                                                                                         191;
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Gerritsen, Mary E.
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Wood, William
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                                                                                                                                                         ; Score 808; DB 9;
; Pred. No. 1.1e-57;
38; Mismatches 140
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                                                                                                                                                                                            Length 473;
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                                                                                                                                                                   84;
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362 432	374	327	314	311	254	255	194	195	134
362 GDAPTEDDYWGGYGGEDQRGEQMCPGAACQAPP 394	374 SGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRL 431	327 SS-NHLYGVAEAGAPPADPSTLYRDLPAEDSRGROG 361	314 GPYHPIWTGRATDEEPLGLPKCCQPDAADKASVLEPGRPASAGNALKGRVPPGDSPPGNG 373	PTRPGSRARGNS 326	YLRINDNEWYCDCRARPLWAWLOKERGSSSEVPCSLPQRLAGRDLKRLAANDLQGCAVAT 313	FIRLNANPWACDCRARPLWAWFQRARVSSSDVTCATPPEROGRDLRALREADFQAC 310	194 PERAFROLHSLDRLLLHONRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAPLRALQ 253	195 TEHVFRGLGSLDRLLLHGNRLOGVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLE 254	134 TLHLDRCGLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHGNRISSV 193

Search completed: April 4, 2003, 12:11:50 Job time : 22 secs

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Search completed: April 4, 2003, 12:10:50 Job time : 50 secs	222 AFRGLSRLTILYLFNNSLASLPGEALADLPSLEFLRLNAN 261	162 LQENSLLHLQDDLFADLANLSHLFLHGNRLRLLTEHVFRGLGSLDRLLLHGNRLQGVHRA 221	102 FRHLQALEELDLGDNRHLRSLEPDTFQGLERLQSLHLYRCQLSSLPGNIFRGLVSLQYLY 161	84

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F;334-357/Domain:
F;358-381/Domain:
F;385-408/Domain:
F;409-432/Domain:
F;440-485/Domain:
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F;226-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;262-309/Domain: proteoglycan carboxyl-terminal homology <PCH>
F;262-309/Domain: proteoglycan carboxyl-terminal homology <PCH>
F;27Binding site: carbohydrate (Thr) (covalent) #status experimental
F;8-21,268-294/Disulfide bonds: #status experimental
F;44,151,234,290/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                      A; Residues: 1-1091 <SUZ>
A; Cross-references: GB:D78572; NID:g1545806; PIDN:BAA11416.1; PID:g1545807
A; Cross-references: GB:D78572; NID:g1545806; PIDN:BAA11416.1; PID:g1545807
C; Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteogl; F; 36-61/Domain: proteoglycan amino-terminal homology <PAH>
F; 71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <IRR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: A58532
R;SUZUKİ, Y.; Sato, N.; Tohyama,
J. Biol. Chem. 271, 22522-22527,
A;Title: cDNA cloning of a novel
A;Reference number: A58532; MUID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glial cell membrane glycoprotein LIG-1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHLEGNKLQVLGKDLLLPQPDLRYLFLNGNKLARVAAGAFQGLRQLDMLDLSNNSLASVP
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                                                          proteoglycan carboxyl-terminal homology
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  12.5%;
27.0%;
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; Pred. No. 1.8e-13;
41; Mismatches 135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M.; Wanaka, A.; Takagi,
  Score
Pred.
  278.5; DB 2;
No. 1.1e-12;
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                      Length 1091;
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t homology <LRR9>
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t homology <LR11>
t homology <LR11>
t homology <LR12>
t homology <LR13>
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homology <LRR7>
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A; Map position: 6q25.3-6q26
C; Superfamily: leucine-rich alpha-2-glycoprotein repeat homology
C; Keywords: hydrolase; metallo-carboxypeptidase
F; 77-100/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1
F; 101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR
F; 125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR
F; 149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR
F; 173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR
F; 173-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRF
F; 221-244/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRF
F; 221-244/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRF
F; 245-268/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRF
F; 293-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRF
F; 317-340/Domain: leucine-rich alpha-2-glycoprotein
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A;Title: The deduced protein sequence of the human carboxypeptidase A;Reference number: A34901; MUID:90094386; PMID:2378615
A;Accession: A34901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lysine carboxypeptidase (EC 3.4.17.3) 83K chain - human C;Species: Homo sapiens (man) C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text C;Accession: A34901
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A;Cross-references: GDB:127893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB:J05158; NID:g179935; PIDN:AAA51921.1; PID:g179936
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A; Residues: 1-536 < TAN>
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В
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                                                           PMLCTCYSSPPTVSCQANNFSSVPLSLPPSTQRLFLQNNLIRTLRPGTFGSN--
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   PMGCDCFVQ--EVFCSDEELATVPLDIPPYTKNIIFVETSFTTLETRAFGSNPNLTKVVF
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                                                                                                                              Conservative
                                                                                                                                                            12.3%;
30.7%;
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                                                                                                                                                            Pred. No.
                                                                                                                                                               Score 273.5; DB 2; Pred. No. 1.1e-12;
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                                                                                                                                     116;
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<LR12>
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neuronal leucine-rich repeat protein-3 - rat C;SpecLes: Rattus norvegicus (Norway rat) C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002 C;Accession: JC7763 R;Fukamachi, K.; Matsuoka, Y.; Kitanaka, C.; Kuchino, Y.; Tsuda, H.
                                                                                       RESULT
JC7763
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R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O. Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs A;Reference number: Z14126; MUID:98360089; PMID:9633030
A;Accession: T13953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: slit protein homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2002
C;Accession: T13953
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Best Local
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                                                                                                                                                        KSKKFR
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                                                                                                                                                                                          READFQ 308
                                                                                                                                                                                                                                                                                       SUVLYGNKITEIPKGLFDGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTI 418
                                                                                                                                                                                                                                                                                                                        HLFLHGNRLRLLTEHVFRGLGSLDRLLLHGNRLQGVHRAAFRGLSRLTILYLFNNSLASL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALRDLEILTLNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTIGQ 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPRNAERLDLDRNNITRITKMDETGLKNLRVLHLEDNQVSVIERGAEQDLKQLERLRLNK 118
                                                                                                                                                                                                                         SKGLFAPLQSIQTLHLAQNPFVCDCHLKWLADYLQDNPIETSGARCSSPRRLANKRISQI 478
                                                                                                                                                                                                                                                         PGEALADLPSLEFLRLNANPWACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDLRAL
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Pred. No. 1.4e-13;
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A;Molecule type: protein
A;Residues: 1-312 <TAK>
A;Residues: 1-312 <TAK>
C;Comment: The function of this plasma protein is not known.
C;Comment: The function of this plasma protein; leucine-rich alpha-2-glycoprotein;
C;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
C;Keywords: duplication; glycoprotein; plasma; tandem repeat
F;58-81/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;82-105/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;106-129/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;130-153/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;178-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
                                                                                                                                                                                                                                                                                                                                                                                                        leucine-rich alpha-2-glycoprotein - human

(;Species: Homo sapiens (man)

C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change

C;Accession: A03211

R;Takahashi, N.; Takahashi, Y.; Putnam, F.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 1906-1910, 1985

Proc. Natl. Acad. Sci. U.S.A. 82, 1906-1910, 1985

A;Title: Periodicity of leucine and tandem repetition of a 24-am

A;Reference number: A03211; MUID:85166241; PMID:3856868

A;Accession: A03211
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A;Title: Rat neuronal leucine-rich repeat protein-3: Cloning and
A;Reference number: JC7763; PMID:11549284
A;Contents: Fibrosarcoma cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Comment: This protein, a new in protein-protein interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-707 <FUK>
A; Cross-references: GB: AF291437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: JC7763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 DTQILLLQTNNIARIEHSTDFPVNLTGLDLSQNNLSSVTNINVQKMSQLLSVYLEENKLT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 MLLALPLAA------PSCPMLCTC-----YSSPPTVSCQANNFSSVPLSLPP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRCDCVIR--WINMNKTNIRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WACDCRARPLWAWFQRARV---SSSDVTCATPPERQGRDLRALREAD-FQACPPAAPTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISIHSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQYLYLQENSLLHLQDDLFADLANLSHLFLHGNRLRLLTEHVFRGLGSLDRLLLHGNRLQ 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSRARGNSSSNHLYGVAEAGAPPADPSTLYRDLPAEDSRGRQGGDAPTEDDYW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLLGLAITALVQAGDKKVDCPQLCTCEIRPWFTPRSIYMEASTVDCNDLGLLNFPARLPA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEILMLGDNPILRIKDMNFQPLLKLRSLVIAGINLTEVPDDALVGLENLESISFYDNRLN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELPEKCLYGLSNLQELYVNHNLLSAISPGAFVGLHNLLRLHLNSNRLQMINSKWFEALPN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----H--LRSLEPDTFQGLERLQSLHLYRCQLSSLPGNIFRGLVS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----APESFPSILDVEADSYVSLHCRATAEPQPEIYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.9%;
22.8%;
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Pred. No. 1.7e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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platelet membrane glycoprotein V precursor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 12-Jan-1993 #sequence_revision 24-Feb-1994 #text_change 05-Nov-1999 C;Date: 12-Jan-1993 #sequence_revision 24-Feb-1994 #text_change 05-Nov-1999 C;Accession: A48030; A60164; A35483; B35483; C35483; A60432; A47507; S34329 C;Accession: A48030; A60164; A35483; B35483; C35483; A60432; A47507; S34329 R;Lanza, F; Morales, M; de La Salle, C; Cazenave, J.P.; Clemetson, K.J.; J. Biol. Chem. 268, 20801-20807, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Molecule type: protein
A;Residues: 365-384, Y, 386-390, (Y, 392-395, Y, 397;188-208, (I, 210;27-50, Y, 52-53;174-
A;Residues: 365-384, Y, 386-390, (Y, 56-57; G, 479-487, Y, 489-498, Y, 500, Y, 502-503, Y, Y, 77, 510-72, YK, 75-77; Y, 56-57; G, 479-487, Y, 489-498, Y, 7500, Y, 7, 502-503, Y, 7, 8, 8, 17; Church, T.A.; McMullen, B.A.; Williams, S.A.
Biochem. Biophys. Res. Commun. 170, 153-161, 1990
A;Title: Human platelet glycoprotein V: a surface leucine-rich glycoprotein related to a A;Reference number: A35483; MUID:90321220; PMID:2372284
A;Recession: A35483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
A60164
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                                                                    A; Map position: 5pter-5qter
C; Superfamily: leucine-rich alpha-2-glycoprotein repeat homology
C; Keywords: blocked amino end; glycoprotein; platelet; tandem re
                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:L11238; NID:g388759; PIDN:AAA03069.1; PID:g388760 C;Comment: This platelet membrane protein is a substrate for thrombin. C;Comment: The amino end of the intact protein is blocked. C;Comment: This protein is absent in Bernard-Soulier syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Molecule type: protein
A; Residues: 477-478, FX', 481-485, 'E', 487, 'V', 489-492, 'NQ', 495, 'E', 497-498
R; Hickey, M.J.; Hagen, F.S.; Yagi, M.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 90, 8327-8331, 1993
A; Title: Human platelet glycoprotein V: characterization of the polypeptic A; Reference number: A47507; MUID:93391348; PMID:7690959
A; Accession: A47507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 121-129, 'W', 131-135; 466-468, 'X', 470 <RO2>
A; Note: this material was designated peptide M393 but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 145-166, 'I', 1
A; Note: this proteolytic
A; Accession: B35483
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A;Accession: A48030
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                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 252-266,'H',268-272,'x',274-279,'I',281-284,'I',286
A; Residues: 257-266,'H',268-272, 'x',274-279,'I',281-284,'I',286
A; Note: this proteolytic fragment was designated peptide M401
R; Zafar, R.S.; Walz, D.A.
                                                                                                                                                                                         A;Cross-references: GDB:230236; OMIM:173511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-560 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
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tle: Platelet membrane glycoprotein V: characterization of the thrombin-sensitive efference number: A60432; MUID:89162331; PMID:2922700

Accession: A60432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,168-169,'X',171-172 <ROT>
c fragment was designated peptide
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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-1531 < NAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           slit-1 protein homolog
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Matches 113; Conservative
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93; Conserv
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Genomics 51, 27-34, 1998
A; Title: Identification of high-molecular-weight proteins A; Reference number: Z14126; MUID:98360089; PMID:9693030
A; Accession: T42218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: MEGF4 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2002
C;Accession: T42218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:AB011530; NID:g3449289; PIDN:BAA32460.1; PID:g3449290 A;Experimental source: strain Sprague-Dawley; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             476 RGPPPRPAADSSSE--APVHPALAPNSSEPWVWAQ-PVTTGKGQD------HSPFWGFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 NNLTHLPKGLLGAQAKLERLLLHSNRLVSLDSGLLNSLGALTELQFHRNHIRSIAPGAFD 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 NANPWACDCRARPLWAWFQR--ARVSSSD-VTCATPPERQGRDLRALREADFQACPPAAP 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRPGSRARGNSSSNHLYGVAEAGAPPADPSTLYRDLPAEDSRGRQGGDAPTEDDYWGGY 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHNSWRCDCGLGPFLGWLRQHLGLVGGEEPPRCAGPGAHAGLPLWALPGGDAE-CP--GP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRGLGKLRQVSLRRNRLRALPRALFRNLSSLESVQLDHNQLETLPGDVFGALPRLTEVLL 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRGLGSLDRLLLHGNRLQGVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLEFLRL 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --SNLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFQGLERLQSLHLY 139
                                                                                                                                                              HVFRGLGSIDRLLLHGNRLQGVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLEFL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLLMLLALPLAAPSCPMLCTCYSSPPTVSCQANNFSSVPLSLPPSTQRLFLQNNLIRTLR
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                                                          RLNANPWACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDLRALREADFQ-----A
                                                                                                            KAFRGATDLKNLQLDKNQISCIEEGAFRALRGLEVLTLNNNNITTIPVSSFNHMPKLRTF
                                                                                                                                                                                                                               RLNRNQLQVLPELLFQNNQALSRLDLSENS:
                                                                                                                                                                                                                                                                                 HLYRCQLSSLPGNIFRGLVSLQYLYLQENSLLHLQDDLFADLANLSHLFLHGNRLRLLTE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LILWAAAWRLGATACPALCTCTGT - - TVDCHGTGLQAIPKNIPRNTERLELN - - - -
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RLHSNHLFCDCHLAWLSQWLRQRPTIGLFTQCSGPASLRGLNVAEVQKSEFSCSGQGEAA
                                                                                                                                                                                                                                                                                                                                                                                              PGTFGSNLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFQGLERLQSL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fruit fly slit protein; EGF homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 310; DB
Pred. No. 7.9e.
51; Mismatches
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8; Mismatches 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
'.9e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162;
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F:101-124/Domain: Proceedylycan animolocy repails
F:101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:173-96/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:173-920/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:288-13/Domain: proteoglycan carboxyl-terminal homology <LRR5>
F:288-13/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:371-994/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F:395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F:494-42/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F:450-494/Domain: proteoglycan amino-terminal homology <PCS2>
12-537/Domain: proteoglycan amino-terminal homology <PCS2>
12-537/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F:572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F:572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F:565-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F:650-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F:651-695/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F:620-643/Domain: proteoglycan amino-terminal homology <PCS3>
F:667-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F:761-695/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F:651-695/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F:651-695/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F:666-690/Domain: leucine-rich
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A;Gene: FlyBase:sli
A;Cross-references: FlyBase:FBgn0003425
A;Introns: 1351/3
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A;Residues: 881-1182,'G',1185-1404,'GT',1463-1464,'YHA' <RO2>
A;Cross references: GB:M23543; NID:g340939; PID:g514357
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C:Species: Drosophila melanogaster
C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
C:Accession: A36665; A31640; S13523
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                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 101
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Residues: 1-1480 <ROT>
Ress-references: GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g8615
Ress-references: GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g8615
Reference: GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g8615
Reference: GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g8615
Reference: GB:X53959; NID:g8614; PID:GAA37910.1; PID:g8615
Reference: Involved in the development of Reference: A31640; MUID:89077533; PMID:3144436
Reference: A31640
89 LFSNNLSTIYPGTFRHLQALEELDLGDN----
                                                                               73 CPRVCSC--TGLNVDCSHRGLTSVPRKISADVERLELQGNNLTVIYETDFQRLTKLRMLQ 130
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                                                                                                                                                                   31 CPMLCTCYSSPPTVSCQANNESSVPLSLPPSTQRLFLQNNLIRTLRPGTFG--SNLLTLW 88
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                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                            14.6%; Score 324.5; DB 2; 23.5%; Pred. No. 6.4e-16; ative 53; Mismatches 122;
    -----RHLRSLEPD---
                                                                                                                                                                                                                                                            Indels 153;
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183 NSLSSLOPGALDDVENLAKFYLDRNQLSSYPSAALSKLRVYEELKLSHNPLKSIPDNAFQ 242	17 LLLMLIALPLAAPSCPMLCTCYSSPPTVSCQANNESSVPLSLPPSTORLFLQNN 70	y Match 14.5%; Score 323; DB 2; Length 361; Local Similarity 28.8%; Pred. No. 1.5e-16; hes 105; Conservative 51; Mismatches 140; Indels 68; Gaps 12;	A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-361 <nea> A;Residues: 1-361 <nea> A;Residues: 1-361 <nea> C;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan carbo C;Keywords: disulfide bond F;300-346/Domain: proteoglycan carboxyl-terminal homology <pch></pch></nea></nea></nea>	ssion: A53860 e, P.J.; Sommarin, Y.; Boynton, R.E.; Heinegard, D. 1. Them. 269, 21547-21554, 1994 e: The structure of a 38-kDa leucine-rich protein (chondroadherin) isolated fro rence number: A53860; MUID:94342341; PMID:8063792 ssion: A53860	05-00-16	300 RALREADEQ 308 491 ESLREEKEK 499	240 ASLPGEALADLPSLEFLRLNANPWACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDL 299	180 NLSHLFLHGKRLRLLTEHVERGLGSLDRLLLHGKRLOGVHRAAFRGLSRLTTILYLFKNSL 239 : : :: ::	73		LHLOD.	126 TFQGLERLQSLHLYRCQLSSLPGNIFRGLVSLQYLYLQENSL	131 LTDNQIHTIERNSFQDLVSLERLDISNNVITTVGRRVFKGAQSLRSLQLDNNQITCLDEH 190

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Fri Apr

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R;Dai, J; Baxter, R.C.

R;Dai, J; Baxter, R.C. Commun. 188, 304-309, 1992

Biochem. Biophys. Res. Commun. 188, 304-309, 1992

A;Title: Molecular cloning of the acid-labile subunit of the rat insulin-1:
A;Teference number: JC1282; MUID:93038676; PMID:1384485

A;Reference number: JC1282; MUID:93038676; PMID:1384485

A;Accession: JC1282

A;Molecule type: mRNA

A;Molecule type: mRNA

A;Cross-references: GB:S46785; NID:9258002; PIDN:AAB23770.2; PID:95705934

A;Cross-references: GB:S46785; NID:9258002; PIDN:AAB23770.2; PID:95705934

A;Experimental source: liver

A;Mote: the authors translated the codon AAG for residue 63 as Arg, AAA for c;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology

C;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology

C;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology

C;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology

C;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology

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s36665
slit protein 2 precursor - fruit fly (I c;Species: Drosophila melanogaster C;Date: 30-Apr-1991 #sequence_revision C;Accession: B36665
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                                                                                                                                                                                                                                                                                                                         {\tt LFQGLSHLWDLNLGWNSLVVLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELD}
                                                                                                                                                                                                                                                                                                                                                     LFADLANLSHLFLHGNRLRLLTEHVFRGLGSLDRLLLHGNRLOGVHRAAFRGLSRLTILY 233
                                                                                                                                                                                                                                                                                                                                                                                                                               -QGSWLRSLEPQALLGLQNLYYLHLERNRLRNLAVGLFTHTPSLASLSLSSNLLGRLEEG
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                                                                                   fruit fly (Drosophila melanogaster)
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Pred. No. 1.5e-16;
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C; Superfamily: fruit fly slit protecin; BGF homology; leucine-rich alpha-2-glycoprotei F; 66-91/Domain: protecoglycan amino-terminal homology <PAHI>F; 66-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>F; 101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>F; 125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>F; 149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>F; 149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>F; 173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>F; 228-272/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>F; 233-313/Domain: protecoglycan amino-terminal homology <PAH2>F; 288-2712/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAR7>F; 347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAR8>F; 371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAR9>F; 419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAR9>F; 419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAR9>F; 419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAR9>F; 512-537/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAR9>F; 512-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAH2>F; 520-643/Domain: leucine-rich alp
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A;Title: slit: an extracellular protein necessary for development of midline A;Reference number: A36665; MUID:91099665; PMID:2176636
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A; Residues: 1-1469 <R
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431 OSLANGTFDAMKSMKTVHLAKNPFICDCNLRWLADYLHKNPIETSGARCESPKRMHRRRI
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                                                         ASLPGEALADLPSLEFLRLNANPWACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDL
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leucine-rich alpha-2-glycoprotein repeat homology
leucine-rich alpha-2-glycoprotein repeat homology
proteoglycan carboxyl-terminal homology <PCS4>
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; Pred. No. 6.3e-16;
53; Mismatches 122;
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A:Reference number: A41915; MUID:92357025; PMID:1379671
A:Accession: A41915
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A; Residues: 1-605 <LEO>
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
C;Accession: A41915
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A;Experimental source: liver
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587 PEVVGLDLRDLSEAHFAPC
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                                                                                                            GLERLWLEGNPWDCGCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPAYTYNNITCASP
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                                        PEROGRDLRALREADFOAC
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                                                                                                                                                                                   SLEFLRLNANPWACDCRARPLWAW------
                                                                                                                                                                                                                                                                                                               NNSLASLPGEALADL-----
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28.8%; Pred. No. 3.
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A;Molecule type: DNA
A;Residues: 1-603 <BOI'>
A;Cross-references: GB:U66900; NID:g1621612; PIDN:AAB17270.1; PID:g1621613
C;Comment: This protein is a serum protein and it is of the ternary complex C;Genetics:
A;Gene: als
A;Map position: 17
                                                                                                                                                                                                                                                         insulin-like growth factor binding complex acid labile chain - mouse C:Species: Mus musculus (house mouse) C:Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 05-Nov-1999 C:Accession: JC6128 R:Boisclair, Y.R.; Seto, D.; Hsieh, S.; Hurst, K.R.; Ooi, G.T. Proc. Natl. Acad. Sci. U.S.A. 93, 10028-10033, 1996 A:Title: Organization and chromosomal localization of the gene encoding the A:Reference number: JC6128; MUID:96413591; pMID:8816745
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A;Residues: 1-420 <mey>
A;Residues: 1-420 <mey>
A;Cross-references: EMBL:Z29083; NID:g435654; PIDN:CAA82324.1; PID:g435655
C;Superfamily: leucine-rich alpha-Z-glycoprotein repeat homology
C;Keywords: duplication; glycoprotein; transmembrane protein
C;Keywords: duplication; glycoprotein; bransmembrane protein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-420/Product: oncofetal trophoblast glycoprotein 5T4 #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 ALPLAAPSCPMLCTCYSSPPTVSCQANNFSSVPLSLPPSTQRLFLQNNLIRTLRPGTFG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLAELQG-----LPHIRVF-LDNNPWVCDCHMADMVTWLKETEVVQGKDRLTCAYPEKMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NRVLLEINSADLD-CDPILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLASLPGEALADLPSLEFLRLNANPWACDCRARPLWAWFQRARV--SSSDVTCATPPERQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LANLSHLELHGNRLRILTEHVERGLGSLDRLLLHGNRLQGVHRAAFRGLSRLTILYLENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPPLAELAALNISGSRLDEVRAGAFEHLPSLRQLDLSHN-PLADLSPFAFSGSNASVSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPSLRHLDLSNNSLVSLTYVSFRNLTHLESLHLEDNALKVLH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPLVELILNHIVPPEDERQNRSFEGMVVAALLAGRALQGLRRLELASNHFLYLPRDVLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --LERLQSLHLY----RCQLSSLPGNIF-----RGLVSLQYLYLQENSLLHLQDDLFAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQPPLPDQCPALCECSEAARTVKCVNRNLTEVPTDLPAYVRNLFLTGNQLAVLPAGAFAR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SNLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFQG------
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                         14.8%;
35.3%;
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Score 329.5; DB 2;
Pred. No. 9.1e-17;
4; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 331.5; DB 2;
Pred. No. 4.2e-17;
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Conservative

34;

Indels

41;

Gaps

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR_73:*

pir1:*
pir2:*
pir3:*
pir4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

30 31 32 33 33 33 33 33 33 33 33 33 33 33 33	ı
232.5 231.5 231.5 231.5 229.5 226.5 224 224 220 220 217.5 206.5 206.5 206.5 204.5	; 1
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1389 626 1389 1385 1385 3562 594 610 738 1016 603 1066)
	د
T10504 T10504 NBHU852 NBHU857 T13887 T34319 T23841 T123836 T1053 T19938 T30553 T1243185 T1243185 T1243185 T1243185))))
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ALIGNMENTS

RESULT 1 JC5239

10	ALREADFQAC 310 DLGEAHFAPC 605	301 596	Qy Db	
NPWACDCRARPLWAWFQRARVSSSDVICATEPERQUARUM 300	NPWACDCRARPLWAW	261 536	Qy Db	
	AAFRGLSRLTILY	221 476	Qy	
GLGSLDRLLLHGNRLQGVHR	YLQENSLLHLQDI : :: : :: FLKDNGLVGIEE(161 416	Qy Db	
GAFLGLTNVAVMNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFAGLSGLRRL 415	GAFLGLTNVAVM	119 356	Qy Db	
WLFSNNLSTIYPGTFRHLQALEELDLGDNR	WLFSNNLSTIYPO	88 296	Qy Db	
GLLEDTFPGLLGLRVL	VPLSLPPSTQRLE: : : : : : LPRLQKLY	54 241	Qy Db	
YSSPPTVSCQANNESS	LPGLRRLLQA : GGLRELVLAGNR	2 193	Qy Db	
9%; Score 353; DB 2; Length 605; 4%; Pred. No. 1.7e-18; 40; Mismatches 130; Indels 138; Ga	Watch 15.1 Local Similarity 28.1 hes 122; Conservative	Query Match Best Local Matches 12	X M O	
structurally related to pro	A;Accession: JC5239 A;Molecule type: mRNA A;Residues: 1-605 C;Comment: This factor is	ccessio plecule esidues omment:	A; Ac A; Mc A; Re C; Cc	
R;Delhanty, P.; Baxter, R.C. R;Delhanty, P.; Baxter, R.C. Biochem. Biophys. Res. Commun. 227, 897-902, 1996 B;Title: The cloning and expression of the baboon acid-labile subunit of the insulin-A;Title: The cloning and expression of the baboon acid-labile subunit of the insulin-A;Title: The cloning and expression of the baboon acid-labile subunit of the insulin-B;Title: The cloning and expression of the baboon acid-labile subunit of the insulin-B;Title: The cloning and expression of the baboon acid-labile subunit of the insulin-B;Title: The cloning acid-labile subunit of the insulin-B	, P.; Baxter, R.C. iophys. Res. Commu he cloning and expe number: JC5239;	R;Delhanty, Biochem. Bio A;Title: The A;Reference A;Contents:	R; De Bioc A; Ti A; Re A; Co	
factor acid-labile chain - baboon . (baboon) #sequence_revision 09-May-1997 #text_change 09-May-1997	growth apio sp or-1997 JC5239	JC5239 insulin-like insulin-like C; Species: Pa C; Date: 17-Ap C; Accession:	JC5239 insuli C; Spec C; Date	

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624 PAQPGDSHLIGAPTSASPYEFSPPGGPVPL 653
              323 RGNSSSNHLYGVAEAG-----APPADPSTL 347
                               568 CDLVPFKQWIE--TISSVSVVGDVLCRSPENLTHRDVRTI-ELEV-LCPEMLHVAPAGES 623
                                                                                               267 CRARPLWAWFQRARVSS----SDVTCATPPERQGRDLRALREADFQACPPAAPTRPGSRA 322
                                                               531 RLNLRKN-----YFLYL-----PVAG-VLEHLNAIVQIDLNENDWDCT 567
                                                                           207 RLLLHGNRLQGVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLEFLRLNANPWACD 266
                                                                                                                                373 CPTGCTCNLHINDLGLTVNCKERGFNNISELLP------RP----RP----LNAKK 412
                                                                                                                                                                           31 CPMLCTC----YSSPPTVSCQANNESSVPLSLPPSTQRLFLQNNLIRTLRPGTFGSNLLT 86
                                                                                                                                                                                                                                        172
197
407
431
455
480
503
528
528
712
977 AA;
                                                                                                                                                                                     195 LR
219 LR
430 LR
454 LR
478 LR
502 LR
5026 LR
5026 LR
723 PPO
109005 MW;
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Search completed: April 4, 2003, 12:08:34 Job time: 18 secs

Lepidosauria; Squamata; Viperidae; Crotalinae; NCBI_TaxID=31147;

; Scleroglossa; Agkistrodon.

Serpentes;

Colubroidea;

93-105; 165-173

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Q
                                 Query Match
Best Local S
Matches 95
                                                                                                                                                                                                                                                                                 Interpro; IPRO00483; LRR_Ctern
Interpro; IPRO00483; LRR_out.
Interpro; IPR003592; LRR_out.
Interpro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 8.
Pfam; PF00463; LRRCT; 1.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00370; LRR; 1.
SMART; SM00382; LRRCT; 1.
SMART; SM00382; LRRCT; 1.
SMART; SM00369; LRRCT; 3.
Signal; Phospholipase A2 inhil
Leucine-rich repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohkura N., Okuhara H., Inoue S., Ikeda K., Hayashi K.;
"purification and characterization of three distinct types of
phospholipase A2 inhibitors from the blood plasma of the Chinese
mamushi, Agkistrodon blomhoffii siniticus.";
Biochem. J. 325:527-531(1997).
-i- FUNCTION: INHIBITS THE ENZYMATIC ACTIVITY OF THE BASIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okumura K., Ohkura N., Inoue S., Ikeda K., Hayashi K.; "A novel phospholipase A2 inhibitor with leucine-rich repeats from the blood plasma of Agkistrodon blomhoffii siniticus. Sequence homologies with human leucine-rich alpha2-glycoprotein."; "J. Biol. Chem. 273:19469-19475(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
177-195; 204-219; 2
                                                                                                                                                                                                                         REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 24-53, CHARACTERIZATION, AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98344034; PubMed=9677367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97361946; PubMed=9230137;
                                                                                                CARBOHYD
CARBOHYD
CONFLICT
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CARBOHYD
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                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB007198; BAA31994.1; -.
                                                                                                                                                                         REPEAT
                                                                                                                                      CARBOHYD
             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MASS SPECTROMETRY: MW-43857.2; MW_ERR=81.9; SIMILARITY: CONTAINS 8 LEUCINE-RICH REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHOLIPASE A2 (PLA2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration
ACLILMELALPLAAPSCPMLCTCYSSPPTVS---CQANNFSSVPLSLPPSTQRLFLQNNL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                      P16473;
                                    Similarity
95; Conserv
                                                                                    45
331 AA;
                                                                                                             1 24
78
78
103
127
150
175
199
223
245
35
125
232
                                     Conservative
                                                                                  ., AND SEQUENCE OF 24-53; 59-87; 225-230; 305-313 AND 317-330.
                                                                                                                                                                                                                                                                                                                                                                                                             LRR_Cterm.
                                                13.9%;
29.1%;
                                                                                                                                                                                                                                                                                                                                                                                    LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                  LRR_out
                                                                                                                                                                                                                                                                                                   inhibitor; Glycoprotein; Repeat;
                                                                                       WW;
                                        47;
                                     Score 309.5;
Pred. No. 3e-1
47; Mismatches
                                                                                                 LRR 2.

LRR 3.

LRR 4.

LRR 5.

LRR 6.

LRR 7.

LRR 8.

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                                                                                       C82FB5DE0E494C46
                                                                                                   NKED (GLCNAC.
L (IN REF. 2
                                                                                                ED (GLCNAC. . .) (POTENTIAL)

D) (GLCNAC. . .) (POTENTIAL)

D) (GLCNAC. . .) (POTENTIAL)

D) (GLCNAC. . .) (POTENTIAL)

CIONEF. 2)

CIONEF. 2)
                                                     3e-15;
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                                                                                                                                                                                                                                                                 A2
                                        148;
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                                        Indels
                                                                 Length
                                                                 331;
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Y848_HUMAN
                                                                                                                                                                                                                                                                            EMBL; AB020655; BAA74871.1; -.
InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
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16-OCT-2001 (
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Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99156230; PubMed=10048485;
Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human
The complete sequences of 100 new cDNA clones from brain v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                              SMART;
                                                                                                                                                                                        Pfam; PF00560; LKK; J.
Pfam; PF01463; LRRCT; 2.
SMART; SM00370; LRR; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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REPEAT
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                                                                                                                           SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             large proteins in vitro.";
Res. 5:355-364(1998).
SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASSLILLPLSENQLAELHPSWFQTLGELRILGLDHNQVKEIPISCFDKLKKLTSLDLSFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                SM00082;
SM00013;
                                                                                                     SM00369; LRR_TYP; 3.
etical protein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 40, Created)
(Rel. 40, Last sequence up)
(Rel. 40, Last annotation)
1 protein KIAA0848.
1 protein;
76 99
100 123
125 147
148 171
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                                                                                                                                                      LRRCT; 2.
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S S E
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     InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_CI
InterPro; IPR000372; LRR_CI
InterPro; IPR003592; LRR_CI
InterPro; IPR003591; LRR_CI
                                                                                              MIM;
                                                                                                                   EMBL; U96769; AAC13410.1; -...
EMBL; U96767; AAC13410.1; JOINED.
EMBL; U96768; AAC13410.1; JOINED.
EMBL; AF371328; AAK51556.1; -...
                                                                                                                                                                                                    entitles requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                            Genew;
                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-98008928; PubMed-9344663;

Grover J., Chen X.-N., Korenberg J.R.,

Grover J., and chromosome location
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAD_HUMAN STANDARD; PRT; 359 AA 015335; 096RJ5; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-21413956; Pubmed-11445564;
                                                                                                                                                                                                                                                                                                                                                                                                                                  MABANSON B., Wenglen C., Moergelin M., Saxne T., Heinegaard D.;

"Association of chondroadherin with collagen type II.";

J. Blol. Chem. 276:3288-32886(2001).

-1- FUNCTION: Promotes attachment of chondrocytes, fibroblasts, and osteoblasts. This binding is mediated (at least for chondrocytes and fibroblasts) by the integrin alpha(2)beta(1). May play an important role in the regulation of chondrocyte growth and proliferation (By similarity).

-1- SUBUNIT: Mostly monomeric (By similarity). Interacts with collage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics [2]
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The structure and chromosome gene (CHAD).";
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                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Extracellular matrix (By similarity). TISSUE SPECIFICITY: Present in chondrocytes at all ages. SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS IV SUBFAMILY. SIMILARITY: CONTAINS 11 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                         type II
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                                                                                                      HGNC:1909; CHAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45:379-385(1997).
                    : LRR_Nterm.
      LRR_typ
                                                       LRR_Cterm
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leucine-rich
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                                                                                                                                                                                                               http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                Usage
                                                                                                                                                                                                                                                                                                                                                                                                                             Interacts with
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RESULT 14
PLIB_AGKBL
ID PLIB_A
AC 093233
DT 30-MAY
DT 30-MAY
DT 15-JUN
DE Phosph
OS Agkist
OS blomho
OC Eukary
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093733;
093733;
30.MAY-2000 (Rel. 39, Created)
30.MAY-2000 (Rel. 39, Last sequence update)
15.JUN-2002 (Rel. 41, Last annotation update)
Phospholipase A2 inhibitor subunit B precurso
AgKistrodon blomhoffii siniticus (Chinese mam
blomhoffii siniticus).
Eukaryota; Metazoa; Chordata; Craniata; Verte
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Best Local S
Matches 104
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Pfam; PF01463; LRRNT; 1.
SMART; SM00370; LRR; 1.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 4.
Signal; Leucine-Tich repeat; R
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DISULFID
DISULFID
DISULFID
CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
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Extracellular
SIGNAL
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REPEAT
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                                                                                                                                                                    PWKCTCQLRGLRRWLE-AKASRPDATCASPAKFKGQHIRDTDAFRSCKF----
                                                                                                                                                                                    PWACDCRARPLWAWFQRARVSSSDVTCATPPERQG---RDLRALREADFQACPPAAPTRP 318
                                                                                                                                                                                                           GRYLETLWLDNTNLEKFSDGAFLGVTTLKHVHLENNRLNQLPSNFPFD-
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                                                                                                                                                                                                                                                                                                                                              RTLRPGTFGS--NLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFQGL
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LRR 11.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

O-LINKED (POPUNTIAL).

V -> L (IN REF. 2).

P -> A (IN REF. 2).

W: 9A318D0A15C157A0 CRC'
Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 313;
Pred. No. 1
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                  (Chinese mamushi)
                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                        update)
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.8e-15;
                            (PLI-B).
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 Euteleostom1;
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Length

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RESULT 12
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16-OCT-2001 (Rel. 40, I
15-JUN-2002 (Rel. 41, I
Glioma amplified on chr
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Glial tumor;
MEDLINE=98324709; PubMed=9662332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAC1
                                                                                                                                                   Malfoy B., Almeida A., Zhu X.X., Vogt N., Tyagi R., Muleris M., Mutrillaux A.-M., Dutrillaux B., Ross D., Hanash S.; "GAC1, a new member of the leucine-rich repeat superfamily on chromosome band 1q32.1, is amplified and overexpressed in malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                            075325;
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                               gliomas.";
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168
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                                                             modified and this statement entities requires a license
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Local Similarity
                        EMBL; AF030435; AAC39792.1;
                                                  or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 KKA 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LILMLLALPLAAP---SCPMLCTCYSSPPTVSCQANNFSSVPLSLPPSTQRLFLQNNLIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSLHPGSLDDVENLAKFHLDRNQLSSYPSAALSKLRVVEELKLSHNPLKSIPDNAFQSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELTYLYLDHNKVSELPRGLLSPLVNLFILQLNNNKIRELRAGAFQGAKDLRWLYLSENAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLQSLHLYRCQLSSLPGNI--------FRGLVSLQYLYLQENSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLAANSFRTVPNLVSLHLQHCNIREVAAGAFRGLKQLIYLYLSHN-DIRVLRAGAFDDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLRPGTFGS--NLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFQGLE 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-LDRLLLHGNRLQGVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLEFLRLNANP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHLQDDLFADLANLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WKCTCQLRGLRRWLE-AKTSRPDATCSSPAKFKGQRIRDTDALR-----SC--KSPTKRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WACDCRARPLWAWFQRARVSSSDVTCATPPERQG---RDLRALREADFQACPPAAPTRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RYLETLWLDNTNLEKFSDAAFAGVTTLKHVHLENNRLNQLPSTFPFD--NLETLTLTNNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106;
              605492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322
 IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                 equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                          40, Last sequence update)
41, Last annotation update)
on chromosome 1 protein prec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.3%; 29.2%;
                                                                                                                                                                                                                                                                                                                                                           Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 318.5; DB 1; Pred. No. 7.4e-16;
                                                                             is not removed.
                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            713
                                                                                                                                                                                                                                                                                                                                                                                                             precursor
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                                                                                Usage
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                                                                                 and
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                                                                                 for
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                                                                                  in no way
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Best I
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SMART; SM00370; LRRC; 1.
SMART; SM00087; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR, TYP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
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CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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REPEAT
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DISULFID
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REPEAT
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin domain;
Leucine-rich repeat; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0019; LEURICHRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
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                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                     180
                                                                                                      154
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                                                                                                                                                         108
                                                  214
                                                                   214
                                  274
334
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                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                              Match
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n; PF01462; LRRNT; 1.
1; PF01463; LRRCT; 1.
                                                                                                                                                                                                          2
                                                                                                                                                                                                                           RLLQAPASACLLLMLLA-----LPLAAPSCPMLCTC-----
                                                                                                                                       LEELDLGDNRHLRSLEPDTEQGLERLQSLHLYRCQLSSLPGNIFRGLVSLQYLYLQENSL
                                                                                                                                                                                         ANNESSYPLSLPPSTORLELONNLIRTLRPGTEGSNLLTLWLESNNLSTIYPGTERHLOA 107
                                                                                                                                                                                                          RLLVAP----LLLAWVAGATAAVPVVPWHVP-CPPQCACQIRPWYTPRSSYREATTVDCN
                                                                                                                                                                                                                                            al Similarity
137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00047; ig;
                                                                                    NLSHLFLHGNRLRLLTEHVFRGLGSLDRLLLHGN-----
                                                                                                     YRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFEMLPNLEILMIGGNKVDAILDMNFRPLA
                                                                                                                                                                         DLFLTAVPPALPAGTQTLLLQSNSIVRVDQSELG---
                                                                   NLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQLARVPRRALEQVPGLKFLDLNKNPL
LPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIRCDCVIR--WANATGTRVRFIE
                LSRLTILYLENNSLASLPGEALADLPSLEFLRLNANPWACDCRARPLWAWFQRARV---S
                                 QRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLPELTKLDITNNPRLSFIHPRAFHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR003598;
IPR001611;
IPR000483;
IPR000372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000372; LRR_Nterm.
IPR003592; LRR_out.
IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                             381
555
583
713
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283
309
334
357
34
357
385
385
497
497
497
555
583
78798 MW;
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652
92
116
140
165
188
213
236
236
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438
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19
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713
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651
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713
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163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal.
                                                                                                                                                                                                                                                      14.18;
24.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                        N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                      Score 314;
Pred. No. 3
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LRR
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LRR
                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
CYTOPLASMIC (POTENTIAL).
LRR 1.
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LRR
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                                                                                                                                                                                                                                                                                                                                                                                             LRR
                                                                                                                                                                                                                                                                                                                         IG-LIKE C2-TYPE
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                           LRR 11
                                                                                                                                                                                                                                                                               -LINKED (GLCNAC. ..) (POTENTIAL).
-LINKED (GLCNAC. ..) (POTENTIAL).
-LINKED (GLCNAC. ..) (POTENTIAL).
-LINKED (GLCNAC. ..) (POTENTIAL).
ECBBCOFD240C9396 CRC64;
                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                         .5e-15
                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                 156;
                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                Length 713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHROMOSOME
                                                                                                                                                                                                                                                Indels 220;
                                                                                                                                                                                                                               ----YSSPPTVSCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat;
                                                       -RLQGVHRAAFRG
                                                                                                                             -----FADLA
                                                                                                                                                                               --YLAN
                                                                                                                                                                                                                                                  Gaps
                                                                                                                             179
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                                                                                                                                                              167
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                                        333
                                                                           273
                       282
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Matches 105;
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Best Local Similarity
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InterPro: IPR000483; LRR_Cterm.
InterPro: IPR000372; LRR. Nterm.
InterPro: IPR0003591; LRR_typ.
Pfam; PF00560; LRR; 10.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01463; LRRNT; 1.
SMART; SM00082; LRRNT; 1.
SMART; SM00082; LRRNT; 1.
SMART; SM00069; LRR_TYP; 5.
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DISULFID
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                          186
                                                                                                                                                      171
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                                                                                                                                                                                                             135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U96626; AAC39963.1; -. EMBL; BC012672; AAH12672.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - - - SIMILARITY: CONTAINS 11 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                      77
                                                                                                                                                                                                                                                                                                                 17 LLLMLLALPLAAPSCPMLCTCYSSPPTVSCQANNESSVPLSLPPSTQRLFLQNNLIRTLR
                                                                                                                                                                                                                                                                                                9
TCQLRGLRRWLE-AKASRPDATCSSPAKFKGQRIRDTDALR-----SC--KSPTKRSKKA
                        DCRARPLWAWFQRARVSSSDVTCATPPERQG----RDLRALREADFQACPPAAPTRPGSRA
                                                                         DRLLLHGNRLQGVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLEFLRLNANPWAC
                                                                                                                                                                     YLYLDHNKVSELÞRGLLSPLVNLFILQLNNNKIRELRAGAFQGAKDLRWLYLSENALSSL
                                                          ETLWLDNTNLEKFSDAAFSGVTTLKHVHLDNNRLNQLPSSFPFD.
                                                                                                                QPGSLDDVENLAKFHLDKNQLSSYPSAALSKLRVVEELKLSHNPLKSIPDNAFQSFGRYL
                                                                                                                                                                                                 SLHLYRCQLSSLPGNI-------FRGLVSLQYLYLQENSLLHL
                                                                                                                                                                                                                              ANSFRTMPNLVSLHLQHCNTREVAAGAFRGLKQLIYLYLSHN-DIRVLRAGAFDDLTELT
                                                                                                                                                                                                                                                          PGTFGS--NLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFQGLERLQ 134
                                                                                                                                                                                                                                                                                     LVFLAILLP-ALAACPQNCHCHGDLQHVICDKVGLQKIP-KVSETTKLLNLQRNNFPVLA
                                                                                                                                                    QDDLFADLANLS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leucine-rich repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                  358
                                                                                                                                                                                                                                                                                                                                                       Conservative
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1 20
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9 72
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216
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29.2%;
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BY SIMILARITY.
BY SIMILARITY.
O-LINKED (POTENTIAL).
GA062FCEBF84A078 CRC64;
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Pred. No. 5.3e
50; Mismatches
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LRR 5.

LRR 6.

LRR 7.

LRR 8.

LRR 9.

LRR 10.

LRR 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHONDROADHERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                           -----HLFLHGNRLRLLTEHVFRGLGS-L
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                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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                                                        -NLETLTLTNNPWKC
                                                                                                                                                                                                                                                                                                                                                 67;
                                                                                                                                                                                                                                                                                                                                              Gaps
                             322
                                                                                    265
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Pfam; PF01162; LRRCT; 1.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRUT; 1.
SMART; SM00369; LRR TYP; 5
                REPEAT
REPEAT
DISULFID
DISULFID
DISULFID
CARBOHYD
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       SEQUENCE
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REPEAT
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REPEAT
                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                  osteoblasts. This binding is mediated (at least for chondrocytes and osteoblasts. This binding is mediated (at least for chondrocytes and fibroblasts) by the integrin alpha(2)beta(1). May play an important role in the regulation of chondrocyte growth and proliferation (By similarity).

1. SUBURIT: Mostly monomeric (By similarity).

1. SUBCELLULAR LOCATION: Extracellular matrix (By similarity).

1. TISSUE SPECIFICITY: Present in femoral head and rib cartilage, as well as in tendon, Detected in bone marrow.

1. SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS

1. SIMILARITY: CONTAINS 11 LEUCINE-RICH REPEATS (LRR).
                                                                                                             REPEAT
                                                                                                                                                                REPEAT
                                                                                                                                                                                   Extracellular matrix SIGNAL 1 :
                                                                                                                                                                                                     Signal; Leucine-rich repeat;
                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            070210;
15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                                                                    REPEAT
                                                                                                                                            REPEAT
                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                             InterPro; IPR000372;
InterPro; IPR003591;
                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                    Pfam; PF00560; LRR; 10
                                                                                                                                                                                                                                                                                                 InterPro; IPR001611;
InterPro; IPR000483;
                                                                                                                                                                                                                                                                                                                         EMBL; AF004953;
                                                                                                                                                                                                                                                                                                                                                                                                between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Chondrosarcoma;
MEDLINE-98129774; PubMed-9461555;
Shen Z., Gantcheva S., Maansson B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Chondroadherin expression changes slochem. J. 330:549-557(1998).
                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                          21
49
73
121
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203
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      AA;
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41, Last sequence up
41, Last annotation
                                                                                                                               358
358
72
96
120
      40403
                                                                                                                                                                                                                                                                            LRR_Nterm.
LRR_typ.
                                                                                                                                                                                                                                                                                                   LRR_Cterm.
     WW.
LRR 11.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
O-LINKED (POTENTIAL).
630946F96F384857 CR
                                                                 POTENTIAL.
CHONDROADHERIN.
                                                                                                                                                                                                   Repeat; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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in skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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development.";
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InterPro; IPR001611; LRR.

InterPro; IPR000483; LRR_Cterm.

InterPro; IPR000372; LRR_Nerm.

InterPro; IPR003592; LRR_out.

R InterPro; IPR003592; LRR_out.

R InterPro; IPR003591; LRR_typ.

Pfam; PF00560; LRR; 13.

R Pfam; PF01463; LRRCT; 1.

R PFINTS; PR00019; LEURICHRPT.

R PRINTS; PR00019; LEURICHRPT.

R SMART; SM000370; LRR; 1.

R SMART; SM000370; LRR, TYP; 9.

R SMART; SM00013; LRRNT; 1.

R SMART; SM00069; LRR_TYP; 9.

W Platelet; Transmembrane; Glycoprotein; Blood coagulation;

W Repeat; Leucine-rich repeat; Cell adhesion; Signal.
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MEDLINE=90321220; PubMed=2372284;
MEDLINE=90321220; PubMed=2372284;
Roth G.J., Church T.A., McMullen B.A., Williams
Roth G.J., church Tlack and Surface leucir
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CONFLICT
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CARBOHYD
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CONFLICT
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SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PLATELETS AND MEGAKARYOCYTES.
PTM: THE N-TERMINUS IS BLOCKED.
SIMILARITY: CONTAINS 14 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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N-LINKED (GLCNAC...)
N-T-> TK (IN REF. 2)
K-> T (IN REF. 2)
N-> W (IN REF. 3)
                                                                                                                                                                                        LRR
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CYTOPLASMIC (POTENTIAL)
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(GLCNAC . . .)
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leucine-rich
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                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
                                                                                                                                                                                                                                                                                                            05522;
05520;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Cartilage leucine-rich
                                                                                                                                                                      Genomics [2]
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Emammalia; Euthoria; Rodentia; Sciurognathi; Muridae; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                          CHAD.
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MEDLINE=98126439; PubMed=9465299;
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                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-Salivary gland;
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                                                                                                                         Submitted
                                                                                                                                    Strausberg R.;
                                                                                                                                                                                                       Landgren C., Beier D.R., E
"The mouse chondroadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                  476
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                                                    mitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
mitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Promotes attachment of chondrocytes, fibroblasts, and stepblasts. This binding is mediated (at least for chondrocytes and fibroblasts) by the integrin alpha(2)beta(1). May play an important role in the regulation of chondrocyte growth and proliferation (By similarity).
SUBUNIT: Mostly monomeric. Interacts with collagen type II (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Extracellular matrix (By similarity). TISSUE SPECIFICITY: Cartilage. SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SIRPS) FAMILY. CLASS IV SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RCQLSSLPGNIFRGLVSLQYLYLQENSLLH-LQDDLFADLANLSHLFLHGNRLRLLTEHV
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                                              similarity).
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13; Conservative
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Best Local Similarity
Matches 105; Conser
                                                                                                                                                                                                                                                                                                                                             Pfam; PF00560; LRR; 10.
Pfam; PF01462; LRRVT; 1.
Pfam; PF01463; LRRCT; 1.
SMART; SM000082; LRRCT; 1.
SMART; SM00013; LRRVT; 1.
SMART; SM00013; LRRVT; 1.
SMART; SM000169; LRR, TYP; 5.
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InterPro; IPR000483; LRR
InterPro; IPR000372; LRR
InterPro; IPR003591; LRR
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17 LLLMLLALPL-----AAPSCPMLCTCYSSPPTVSCQANNESSVPLSLPPSTQRLELQNN 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hu B., Coulson L., Moyer B., Price P.A.;
"Isolation and molecular cloning of a novel bone phosphoprotein related in sequence to the cystatin family of thiol protease inhibitors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE OF 25-55 AND 77-97.
TISSUE-Bone;
MEDLINE-95113864; PubMed-7814406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: Cartilage.
SIMILARITY: BELONGS TO THE SMALL I
(SLRPS) FAMILY. CLASS IV SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Promotes attachment of chondrocytes, fibroblasts, and osteoblasts. This binding is mediated (at least for chondrocytes and fibroblasts) by the integrin alpha(2)beta(1). May play an important role in the regulation of chondrocyte growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 11 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proliferation.
SUBUNIT: Mostly monomeric. Interacts with collagen type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chem. 270:431-436(1995)
                                                                      361 AA;
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                      ne-rich repeat;
                                                                                                                                                                                                                                                                                                                               matrix
                                                                                 348
328
146
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361
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                                      14.6%;
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                           51;
                                                                             O-LINKED (POTENTIAL).
C -> Y (IN REF 2).
C -> W (IN REF 2).
C -> H (IN REF 2).
C -> H (IN REF 2).
C -> L (IN REF 2).
S -> R (IN REF 2).
                       Score 324; DB 1;
Pred. No. 3e-16;
51; Mismatches 140
                                                                                                                                                                  LRR
BY S
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LRR 2.
LRR 3.
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                                                                   DA79DC98AD3DD1F8
                                                                                                                                                                SIMILARITY.
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                         140;
                                             Length 361
                                                                  CRC64;
                         Indels
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                       68;
                     Gaps
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RESULT 5
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ID GPV_HUMAN
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                                                                                                                                         PARTIAL DESTRUCTION OF TISSUE-platelet;
MEDLINE-90275263; PubMed-2350580;
Shimomura T., Fujimura K., Maehama
Shimomura T., Oyama R., Suzuki M., J
                                                                                                                                                                                                                                                                                      MEDIJINE-94012616; PubMed-8407908;
Lanza F., Morales M., de la Salle C., Cazenave J.-P., Clemetson K.J.,
Shimomura T., Phillips D.R.;
"Cloning and characterization of the gene encoding the human platelet
glycoprotein V. A member of the leucine-rich glycoprotein family
cleaved during thrombin-induced platelet activation.";
J. Biol. Chem. 268:20801-20807(1993).
                                                     "Rapid purification and characterization of human glycoprotein V: the amino acid sequence contains 1 repetitive modules as in glycoprotein Ib.";
PARTIAL SEQUENCE
                                                Blood 75:2349-2356(1990)
                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE.
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Hickey M.J., Hagen F.S., Yagi M., Roth G.J.;
"Human platelet glycoprotein V: characterization of and the related Ib-V-IX receptor system of adhesive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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01-FEB-1995 (Rel. 31, Last seq)
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Platelet;
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Primates;
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Last annotation update)
V precursor (GPV) (CD42D).
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Icihara-Tanaka
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SITE; PS001185; CTCK_1
SSITE; PS00125; CTCK_2
COSITE; PS00122; EGF_1
/COSITE; PS01186; EGF_1
/COSITE; PS01187; EGF
PROSITE; PS01187; EGF
PROSITE; PS01025; LA
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B5; CTCK_1; 1.
25; CTCK_2; 1.
22; EGF_1; 7.
B6; EGF_2; 5.
B7; EGF_CA; 2.
B8; EGF_CA; 2.
25; LAM_G_DOMAIN; 1.
25; LAM_G_DOMAIN; 1.
25; LAM_G_DOMAIN; 1.
26; Repeat; Leucine-rich repeat.
    LRR 22.
LRR 23.
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EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
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CHAD_BO
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          Query Match
Best Local
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                                                                                                                                                                                  CHAD_BOVIN
Q27972;
Q1-NOV-1997
Q1-NOV-1997
Q1-NOV-1997
                                                                                                                                                                                                                                        _BOVIN
                                                                                                                                                    protein).
                                                                                     воvidae; Bovinae; Bos. NCBI_TaxID=9913;
         TISSUE-Cartilage;
MEDLINE=94342341; PubMed=8063792;
Meame P.J., Sommarin Y., Boynton R.E., Formarin P.J., Biolated from bovine cartilage.";
J. Biol. Chem. 269:21547-21554(1994).
                                                                                                                                                                          Chondroadherin
                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                         SEQUENCE FROM N.A.,
                                                                                                                                          Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                311
                                                                                                                                                                                                                                                                                                                                                                                                                                     173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101;
                                                                                                                                           (Bovine).
                                                                                                                                                                       (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
(Rel. 41, Cartilage leucine-rich
```

STANDARD;

PRT;

361

ΑA

protein)

(38 kDa

bone

Chordata; Craniata; Vertebrata; Eute Cetartiodactyla; Ruminantia; Pecora;

Euteleostomi;

Bovoidea

AND

PARTIAL

SEQUENCE

Heinegaard

D.

protein

(chondroadherin)

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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPMICTCYSSPPTVSCQANNESSVPLSLPPSTQRLFLQNNLIRTLRPGTFG--SNLLTLW
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                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt LAPYTRCQSPSQLKGQNVADLHDQEFKCSGLTEHAPMECGAENSCPHPCRCADGIVDCRE}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTDNQIHTIERNSFQDLVSLERLDISNNVITTVGRRVFKGAQSLRSLQLDNNQITCLDEH
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ESLREEKFK
                                                RALREADFQ
                                                                                                    ASLPGEALADLPSLEFLRLNANPWACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDL
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Pred.
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Matches
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Pfam; PF00465; LRRNT; 1.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01463; LRCT; 1.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00370; LRR; 5.
SMART; SM00303; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
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PIR; JC1282; JC1282.
InterPro; IPR001611;
InterPro; IPR000483;
InterPro; IPR00372;
InterPro; IPR003592;
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SIGNAL
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LSRNALRSVKANVFVHLPRLQKLYLDRN 252
                                                                GDNRHLRSLEPDTFQGLERLQSLHLYRCQLSSLPGNIFRGLVSLQYLYLQENSLLHLQDD
                                                                                              VPLSLPPSTQRLFLQNNLIRTLRPGTFGSNLLTLWLFSNNLSTIYPGTFRHLQALEELDL
:! :| :| :| :| :| :| :| :| :| :| :|
                                                                                                                                PASACLLLMLLAL------PLAA-----PSCPMLCTC----YSSPPTVSCQANNFSS
              LFNNSLASLPGEALADLPSLEFLRLNAN 261
                          LFQGLSHLWDLNLGWNSLVVLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELD
                                        LFADLANLSHLFLHGNRLRLLTEHVFRGLGSLDRLLLHGNRLQGVHRAAFRGLSRLTILY
                                                                                                                 PALVVLLAFWVALGPCHLQGTDPGASADAEGPQCPVACTCSHDDYTDELSVFCSSKNLTH
                                                        -QGSWLRSLEPQALLGLQNLYYLHLERNRLRNLAVGLFTHTPSLASLSLSSNLLGRLEEG
                                                                                        LPDDIPVSTR-----
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SM00369;
                                                                                                                                                         Similarity
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144
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35.18;
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LRR_out.
LRR_typ.
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Pred. No. 3.7e
95; Mismatches
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LRR 19
LRR 20
LRR 21
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nes 98;
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                                                                                                                                               Gaps
                                          233
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RESULT 7

SLIT_DROME
ID T_LDROME
ID SLIT_DROME
AC P24014
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CC -1- WI
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P24014;
01-MAR-1992 (Rel. :
01-MAR-1992 (Rel. :
15-JUN-2002 (Rel. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MATRIX MOLECULES: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

1 TISSUE SPECIFICITY: EXCRETED BY THE MIDLINE GLIA CELLS AND EVENTUALLY DISTRIBUTED ALONG THE AXONS.

1 SIMILARITY: CONTAINS 7 EGF-LIKE DOMAINS.

1 SIMILARITY: CONTAINS 24 LEUCINE-RICH REPEATS (LRR).

1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE (CTCK) DOMAIN.

1 SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glia and domains."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0003425; InterPro; IPR000152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A36665; A36665
HSSP; P00740; 1EDM.
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Eukaryota; Metazoa; Arthropoda; Man
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FUNCTION: NECESSARY FOR DEVELOPMENT OF MIDLINE GLIA AND COMMISSURAL AXON PATHWAYS. SLIT MAY INTERACT WITH EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                             PF00007;
                                                                                                                                                                                                                                                                                                                     PF00054;
PF00560;
PF01462;
SM00041;
SM00179;
SM003701;
SM00382;
SM00082;
SM00013;
SM00013;
SM000369;
SM000282;
                                                                                                                                                                                                                                                                                   PF01463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rg J.M., Jacobs J.R., Goodman C.S., Artavanis-Tsakonas
an extracellular protein necessary for development of
nd commissural axon pathways contains both EGF and LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A36665.
                                                                                                                                                                                                                                                                            LRRY 16.
                                                               CT; 1.
EGF_CA; 2.
EGF_like; 5.
LRR; 4.
LRRCT; 4.
LRRNT; 4.
                                                                                                                                                                                                                                                                                                                                                                                    laminin_G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cys_knot;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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21, Last sequence up
41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed-2176636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asx_hydroxyl.
Cys_knot.
EGF-like.
EGF_2.
EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRR.Cterm.
LRR_Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laminin_G
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the Europuse by
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Boisclair Y.R., Seto D., Hsteh S., Hurst K.R.,
"Organization and chromosomal localization of
mouse acid labile subunit of the insulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restrained the Entropean Bioinformatics Institute.
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                                                 REPEAT
CARBOHYD
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REPEAT
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SMART; SM00369; LRR_TYP;
                                                                                                                                                                                                                                                                                      PRINTS; PRO0019; LEURICHRPT SMART; SM00370; LRR; 4. SMART; SM00082; LRRCT; 1.
                                                                                                                                                                                                                                                                                                              Pfam; PF00560; LRR; 19
Pfam; PF01462; LRRNT;
Pfam; PF01463; LRRCT;
                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
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CARBOHYD
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REPEAT
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REPEAT
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EUNCTION: MAY HAVE AN IMPORTANT ROLE IN REGULATING :
EUNCTION: GIGES TO THE TISSUES.

SUBUNIT: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 150
IGF-I OR IGF-I AND IGFBP-3 (BY SIMILARITY).

SUBCELLULAR LOCATION: EXTRACE!LULAR.

SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                 ; U66900; AAB17270.1; -. MGI:107973; Igfals.
52
74
98
121
146
                                                                                                                                                                                                                                                               Leucine-rich
                                                                                                                                                                                                                                                603
 19
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                                                                                                                                                                                                                                                       repeat; Repeat; Signal.
BY SIMILARITY.
                                                          Sciurognathi; Muridae; Murinae; Mus
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                       LRR
LRR
LRR
                                                                                                                                                                                                                              INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN.
                                          N-LINKED
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Best Local
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P35859;
                                                                                                                                                                                                                                                                                                       "Purification and characterization of the acid-labile subunit serum insulin-like growth factor binding protein complex."; Endocrinology 134:848-852(1994).

-i- FUNCTION: MAY HAVE AN IMPORTANT ROLE IN REGULATING THE ACC CIRCULATING IGFS TO THE TISSUES.

-i- SUBUNIT: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 150 kDa W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    precursor (ALS).
IGFALS OR ALS.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Insulin-like growth factor binding protein complex acid labile chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         growth factor binding protein complex."; Biochem. Biophys. Res. Commun. 188:304-309(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Wistar; TI
MEDLINE=94130835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restricted that the content of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baxter R.C., Dai J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 24-44, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dai J., Baxter R.C.;
"Molecular cloning of the acid-labile subunit of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93038676;
entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                               use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 DLSRNALRSVKANVFIHLPRLQKLYLDRN 252
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                                                                                                                                                                                                                                           SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: BF
                                                                                                                                                                                               SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LRR).
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                                                                                                                                                                                                                                                                                           OR IGF-II AND IGFBP-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Serum;
35; PubMed=7507839;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=1384485;
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Rodentia;
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BRAIN, KIDNEY, I
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Pred. No. 2.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                LUNG, HEART,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .3e-16;
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                                                                                                                                 EMBL outstation
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                                                                                                                                      a collaboration
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RESULT 4
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R InterPro; IPR000483; LRR_term.
R InterPro; IPR000483; LRR_term.
R InterPro; IPR000372; LRR_Nterm.
R InterPro; IPR0003592; LRR_out.
R InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 12.
R Pfam; PF01463; LRRCT; 1.
R Pfam; PF01463; LRRCT; 1.
R PRINTS; PR00019; LEURICHRPT.
R SMART; SM00370; LRR; 1.
R SMART; SM000370; LRR; 1.
R SMART; SM00013; LRRCT; 1.
R SMART; SM00013; LRRCT; 1.
R SMART; SM00016; LRRCT; 1.
R SMART; SM00016; LRRCTY; 1.
R SMART; SM00016; LRRCTYP; 10.
R Platelet; Transmembrane; Glycoprotein; Blood coagulation;
W Platelet; Leucine-rich repeat; Cell adhesion; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A RAVENARE C., MOTALES M., AZOTSE D.O., MOOG S., Schuhler S.,

(A Grunert P., Loew D., van Dorsselaer A., Cazenave J.-P., Lanza F.;

(T) Gene cloning of rat and mouse platelet glycoprotein V:

(T) Identification of megakaryovyte-specific promoters and demonstration

(T) of functional thrombin cleavage.";

(L) Elood 89:3253-3262(1997).

(C) INUCTION: THE GPIB-V-IX COMPLEX FUNCTIONS AS THE VON WILLEBRAND

(C) FACTOR RECEPTOR AND MEDIATES VON WILLEBRAND FACTOR-DEPENDENT

(C) FACTOR RECEPTOR AND MEDIATES VON WILLEBRAND FACTOR PLATELETS TO

(C) INUURED VASCULAR SURFACES IN THE ARTERIAL CIRCULATION IS A

(C) CRITICAL INITIATING EVENT IN HEMOSTASIS (BY SIMILARITY).

(1- SUBCELLULAR LOCATION: Type I membrane protein.

(1-) SIMILARITY; CONTAINS 14 LEUCINE-RICH REPEATS (LRR).
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008742;
15-JUL-1998
15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 269595; CAA93441.1; -. HSSP; P09661; 1A9N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6; TISSUE-Liver; MEDLINE-97275136; PubMed=9129
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Mammalia; Eutheria;
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(Rel. 36, Last sequence update)
(Rel. 40, Last annotation updat
ycoprotein V precursor (GPV) (CD
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precursor (ALS)
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STRAIN-Wistar; TISSUE=Liver;
MEDLINE=97275136; PubMed=9129030;
Ravanat C., Morales M., Azorsa D.O., Moog S., Schuhler S.,
Grunert P., Loew D., van Dorsselaer A., Cazenave J.-P., Lanza
"Gene cloning of rat and mouse platelet glycoprotein V:
identification of megakaryocyte-specific promoters and demonsi
                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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                                                        SEQUENCE FROM N.A
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36, Last sequence update)
40, Last annotation update)
tein V precursor (GPV) (CD42)
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282 PEVLFGEMAGLRELWLNGTHLRTLPAAAFRNLSGLQTLGLTRNPLLSALPPGMFHGLTEL

EPDTFQGLERLQSLHLYRCQLSSLPGNIFRGLVSLQYLYLQENSLLH-LQDDLFADLANL

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Matches 109
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Pfam; PF01463; LRCT; 1.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00370; LRR; 2.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
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1. SM0370; LRRCT; 1.

1. SM00082; LRRCT; 1.

1. SM00082; LRRCT; 1.

1. SM00369; LRRCT; 10.

1. SM00369; LRRCTY; 10.

1. SM00369; LRRCTY; 10.

1. SM00369; LRRCTY; 10.

1. SM00369; LRRCT; 10.

1. SM00370; LRRCT; 10.

1. SM00082; LRRCT; 10.

1. SM00084; LRRCTT; 10.

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                                        LFLQNNLIRTLRPGTFGS--NLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSL
LRLERNHLRSIAPGAFDSLGNLSTLTLSGNLLESLPPALFLHVSWLTRLTLFEN-PLEEL
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IPR003592;
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Pfam; PF00560; LRR; 19. Pfam; PF01462; LRRWT; 1.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01463; LRRCT; 1.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00080; LRRCT; 1.
SMART; SM00081; LRRCT; 1.
SMART; SM00013; LRRWT; 1.
SMART; SM00013; LRRWT; 1.
SMART; SM00013; LRRTYP; 11.
Clycoprotein; Leucine-rich regional
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-!- SUBUNIT: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 150 kDa WITH IGF-I OR IGF-II AND IGFBP-3.

-!- TISSUE SPECIFICITY: PLASMA.

-!- TISSUE SPECIFICITY: PLASMA.
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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Baxter R.C., Martin J.L., Beniac V./
"High molecular weight insulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complex. Purification
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Mammalia; Eutheria; Primates;
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); IPR000372; LRR_
); IPR003592; LRR_
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r R.C., Camerato T.,
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PROPEIN (LRR 1. LRR 2. LRR 3. LRR 4. LRR 5. LRR 6. LRR 6. LRR 7. LRR 7. LRR 9.
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GenCore version $5.1.4_p5_4578$ Copyright (c) 1993 - 2003 Compugen Ltd.

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Perfect score:
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and is derived by analysis of the total score distribution.
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GARP_HUMAN
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Signal Signowith	baboon acid-labile su protein complex."; :897-902(1996). **-ROTEIN INTERACTIONS T *-LIGAND BINDING OR CEL EX OF ABOUT 140 TO 150 BY SIMILARITY). Ilular. IB-RICH REPEATS (LRR). IB-RICH REPEATS and the coinformatics and the cute. There are no re as long as its conter as long as its conter	update) on update) protein complex acid labile ch pratein complex acid labile ch protein complex acid labile ch	AA.	
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GENERAL INFORMATION:
APPLICANT: Rothbe
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 800 Kb
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 6.0.5
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/09055
FILING DATE: 19911127
CLASSIFICATION: 435
     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/624,135
FILING DATE: 7-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barth, Richard J.
REGISTRATION NUMBER: 28,180
REFERREZ/DOCKET NUMBER: 900964/RSB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 972-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 14.6%; Score 324.5; DB 4; Best Local Similarity 23.5%; Pred. No. 1.1e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rothberg, Jonathan Marc and Artavanis-Tsakonas, Spyridon TITLE OF INVENTION: purified SLIT protein and Sequence Elements Then NUMBER OF SEQUENCE: 9
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Yale University
ADDRESSEE: Office of Cooperative Research
STREET: 246 Church Street
STREET: Suite 401
CITY: New Haven
STATE: Connecuticut
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 LAPYTRCQSPSQLKGQNVADLHDQEFKCSGLTEHAPMECGAENSCPHPCRCADGIVDCRE 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 AFKGLVELEILTLNNNNLTSLPHNIFGGLGRLRALRLSDNPFACDCHLSWLSRFLRSATR 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 LTDNQIHTIERNSFQDLVSLERLDISNNVITTVGRRVFKGAQSLRSLQLDNNQITCLDEH 190
                                                                                                                                                                                                                                                                                                                         ZIP: 06510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 CPMLCTCYSSPPTVSCQANNESSVPLSLPPSTQRLFLQNNLIRTLRPGTFG--SNLLTLW 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSLANGTFDAMKSMKTVHLAKNPFICDCNLRWLADYLHKNPIETSGARCESPKRMHRRRI 490
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TELEX: 236268
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1480 amino acid
TYPE: AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                431 QSLANGTFDAMKSMKTVHLAKNPFICDCNLRWLADYLHKNPIETSGARCESPKRMHRRRI
    491
                                            300 RALREADFO 308
                                                                                                                                                                     311 KSLTSVPVTLPDDTTDVRLEQNFITELPPKSFSSFRRLRRIDLSNNNISRIAHDALSGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                    180 NLSHLELHGNRLRLLTEHVFRGLGSLDRLLLHGNRLQGVHRAAFRGLSRLTILYLFNNSL 239
                                                                                                                                                                                                                                                                                                                                                    251 LAPYTRCQSPSQLKGQNVADLHDQEFKCSGLTEHAPMECGAENSCPHPCRCADGIVDCRE 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 CPMLCTCYSSPPTVSCQANNESSVPLSLPPSTQRLFLQNNLIRTLRPGTFG--SNLLTLW 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD: similarity to epidermal growth OTHER INFORMATION: Involvement in receptor-ligand NAME/KEY: Alternative splice segment LOCATION: 1394 to 1404
IDENTIFICATION METHOD: experimental OTHER INFORMATION: developmentally regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: COOH-terminal region LOCATION: 1405 to 1480 IDENTIFICATION METHOD: experime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 23.5 ses 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION METHOD: similarity to tandem EGF-like OTHER INFORMATION: protein-protein interactions NAME/KEY: 7th EGF-like repeat LOCATION: 1353 to 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Tandem EGF-like repeats LOCATION: 911 to 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION METHOD:
OTHER INFORMATION: med
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Four Flank-LRR-Flank domains LOCATION: 37 to 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD: similarity to other signal OTHER INFORMATION: Directs Export
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: signal sequence LOCATION: 1 to 36
ESLREEKFK
                                                                                                                        ASLPGEALADLPSLEFLRLNANPWACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDL 299
                                                                                                                                                                                                                                                                                                         ------DLFADLA 179
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AMINO ACIDS
OGY: Linear
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    Score 324.5; DB 5; Length 1480;
    Pred. No. 1.1e-21;
    Mismatches 122; Indels 153;

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2003, 12:11:25

US-09-540-245A-7

GENERAL INFORMATION:

Sequence 7, Application US/09540245A Patent No. 6270984

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                                 Sequence 7, Application US/09540153
Patent No. 6270995
GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
APPLICANT: Krose, Katja
APPLICANT: Tessier-Lavigne, Marc
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CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 60/061,057
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
COUNTAINS DATASETT VA-
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TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
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EQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1480
TYPE: PRT
ORGANISM: Drosophila melanogaster
APPLICANT: Tessier-Lavigne, Marc TITLE OF INVENTION: Modulating Robo: FILE REFERENCE: B98-031-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 LTDNQIHTIERNSFQDLVSLERLDISNNVITTVGRRVFKGAQSLRSLQLDNNQITCLDEH 190
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                                                                                                                                                                                                                                                                                RALREADFQ 308
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                                                                                                                                                                                                                                                                                                                                                       ASLPGEALADLPSLEFLRLNANPWACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDL
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23.5%; Pred. No. 1.1e
tive 53; Mismatches
                   Ligand Interactions
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1.1e-21;
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, ORGANISM: Drosophila melanogaster US-09-540-153-7
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US-09-182-024A-5
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Matches
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SEQ ID NO 7
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PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
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CURRENT FILING DATE: 2000-03-31
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PRIOR FILING DATE: 1998-11-13
                                                  SOFTWARE:
SEQ ID NO 5
                                                                                                                      APPLICANT: Connolly, Timothy
APPLICANT: Rajput, Bhanu
TITLE OF INVENTION: Human Slit Polypeptide and Polynucleotides Encoding
TITLE OF INVENTION: Same
TITLE OF INVENTION: Same
FILE REFERENCE: 640100-271
CURRENT APPLICATION NUMBER: US/09/182,024A
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/063,946
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/096,420
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                                                                     NUMBER OF SEQ ID NOS: SOFTWARE: Patentin V
                                                                                                         PRIOR FILING DATE:
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ORGANISM: Drosophila melanogaster
               TYPE: PRT
                                   LENGTH: 1480
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                                                                                                           1998-08-13
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Pred. No. 1.1e-21;
3; Mismatches 122;
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US-08-487-072A-50
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                                                                                                                                                                                          Matches
                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 887-076
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MURASHIGE KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: WD-40 - Derived Peptides and TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mochly-Rosen, Daria APPLICANT: Ron, Dorit
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114 GDNRHLRSLEPDTFQGLERLQSLHLYRCQLSSLPGNIFRGLVSLQYLYLQENSLLHLQDD 173
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                                                                                                                                                  12 PASACLLLMLLAL------PLAA-----PSCPMLCTC----YSSPPTVSCQANNFSS 53
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CITY: Washington
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                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                      LPDDIPVSTR-----
                                                                                   VPLSLPPSTQRLFLQNNLIRTLRPGTFGSNLLTLWLFSNNLSTIYPGTFRHLQALEELDL 113
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                                                                                                                     PALVVLLAFWVALGPCHLQGTDPGASADAEGPQCPVACTCSHDDYTDELSVFCSSKNLTH 67
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202) 887-0763
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pro. complex-rat, Fig. 33
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                                                                                                                                                                                      Score 326.5; DB 4;
Pred. No. 1.9e-22;
5; Mismatches 98;
                                                  -----ALWLDGNNLSSIPSAAFQNLSSLDFLNL 105
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APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/191,647
CURRENT FILING DATE: 1998-11-13
EARLIER APPLICATION NUMBER: 60/065,544
EARLIER APPLICATION NUMBER: 60/065,544
EARLIER FILING DATE: 1997-11-14
EARLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
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US-09-191-647-7
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APPLICANT: GOOdman, Corey
APPLICANT: Kld, Thomas
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                       191 AFKGLVELEILTLNNNNLTSLPHNIFGGLGRLRALRLSDNPFACDCHLSWLSRFLRSATR 250
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  ESCREEKFK 499
                                        RALREADFQ 308
                                                                                                                        ASLPGEALADLPSLEFLRLNANPWACDCRARPLWAWFQRARVSSSDVTCATPPERQGRDL 299
                                                                                                                                                                QLTTLVLYGNKIKDLPSGVFKGLGSLRLLLLNANEISCIRKDAFRDLHSLSLLSLYDNNI 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CPRVCSC--TGLNVDCSHRGLTSVPRKISADVERLELQGNNLTVIYETDFQRLTKLRMLQ 130
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                                                                                QSLANGTFDAMKSMKTVHLAKNPFICDCNLRWLADYLHKNPIETSGARCESPKRMHRRRI
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                                                                                                                                                                                                                                  ANTI-SENSE:
                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/487,072 FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 07-JUN-
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MURASHIGE, KATE REGISTRATION NUMBER: 2
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OPERATING SYSTEM: PC-DOS/MS-DOS
           54 VPLSLPPSTQRLFLQNNLIRTLRPGTFGSNLLTLWLFSNNLSTIYPGTFRHLQALEELDL 113
                                                                           12 PASACLLLMLLAL------PLAA-----PSCPMLCTC----YSSPPTVSCQANNFSS 53
                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/477,346
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                                            PALVVLLAFWVALGPCHLQGTDPGASADAEGPQCPVACTCSHDDYTDELSVFCSSKNLTH 67
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NO
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202) 887-0763
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N: 514
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pro. complex-rat, Fig. 33
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                                                                                                                        Score 326.5;
Pred. No. 1.
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98;
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                                                                                                                                                     Query Match
Best Local 9
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                                                                                                                                       Matches
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INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                   TYPE: amino a TOPOLOGY: unk MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mochly-Ro
APPLICANT: Ron, Dori
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PATENTIN Rel.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILLING DATE: 07-JUN-19
                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
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ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Morrison & .... AVenue, STREET: 2000 Pennsylvania Avenue,
68 LPDDIPVSTR---
                   54 VPLSLPPSTQRLFLQNNLIRTLRPGTFGSNLLTLWLFSNNLSTIYPGTFRHLQALEELDL 113 :| :| :| :| :| :| :| 113
                                                                                              12 PASACILIMILAL------PIAA-----PSCPMICTC----YSSPPTVSCQANNESS 53
                                                                                                                                                     Local Similarity
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                                                                 PALVVLLAFWVALGPCHLQGTDPGASADAEGPQCPVACTCSHDDYTDELSVFCSSKNLTH 67
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5. 6342368
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                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                        unknown .
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                                                                                                                                                                                                                       Insulin-like growth factor bind.
pro. complex-rat, Fig. 33
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                                                                                                                                                       Score 326.5; DB 4
Pred. No. 1.9e-22;
                                                                                                                                       Mismatches
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-ALWLDGNNLSSIPSAAFQNLSSLDFLNL 105
                                                                                                                                                                     DB 4;
                                                                                                                                       98;
                                                                                                                                                                   Length 603;
                                                                                                                                       Indels
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	Oy 201 GLGSLDRLLLHGNRLQGV	0
	Db 348 NOLOEVKAGAFLGLTNVAVMNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFT 407	-
	VSLQYLYLQENSLLHLQDD	0
	ASLRPRTFKDLHFLEELQLGHNR	п
	FOGLER	_
	LDR	_
	Qy 47 QANNESSVPLSLPPSTQRLFLQNNLIRTLRPGTFGS82	_
86	Query Match 15.7%; Score 349; DB 4; Length 605; Best Local Similarity 28.8%; Pred. No. 1.5e-24; Matches 109; Conservative 33; Mismatches 115; Indels 122; Gaps	
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	INDIVIDUAL ISOLATE: Insulin-like growt	
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	MOLECULE TYPE: protein HYPOTHETICAL: NO	
	GY: unk	
	: LENGTH: 605 amino acids	
	SEQUENCE CHARACTERISTICS:	
	(202) 887-0763	
	TELEPHONE: (202) 887-1500	
	REFERENCE/DOCKET NUMBER: 2550-0025.20	
	ATTORNEY/AGENT INFORMATION:	
	; FILING DATE: 07-JUN-1995 ; CLASSIFICATION: 514	
	APPLICATION NUMBER: US/08/487,072A	
	; SOFTWARE: PatentIn Release #1.0, Version #1.25	
	SYSTEM: PC-DOS/MS-DOS	
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	ER READABL	
	; COUNTRY: USA	
	STATE: DC	
	2000 Pennsylvania	
	E: Morrison & Foel	
	ENCES:	
	APPLICANT: Ron, Dorit	
	TCANT: MOCHIVEROSON	
	Pa	
	Secuence 49 Application	
	Db 587 PEVVGLDLRDLSEAHFAPC 605	
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	h 14.7%; Score 326.5; DB 1; Length 603; Similarity 35.1%; Pred. No. 1.9e-22; 94; Conservative 35; Mismatches 98; Indels 41; Gg SACLLIMILALPLAAPSCPMLCTCYSSPPTVSCQANNFSS	GLSGLERLETKDNGLVGIEEOSLAGLAELLELDLTSNOLTHLPHR-LFOGLGKLEYLLLS NNSLASLPGEALADL

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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
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LENGTH: 605 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 887-1500
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MEDIUM TYPE: Floppy disk
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HYPOTHETICAL:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                47 QANNFSSVPLSLPPSTQRLFLQNNLIRTLRPGTFGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                              --NLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFQGLERLQSLHLYR 140
   PERQGRDLRALREADFQAC
                                                                                                                          NNSLASLPGEALADL ----
                                                                                                                                                        GLSGLRRLFLKDNGLVGIEEQSLWGLAELLELDLTSNQLTHLPHR-LFQGLGKLEYLLLS 466
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                                                                                                                                                                                                                      NQLQEVKAGAFLGLTNVAVMNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFT 407
                                GLERLWLEGNPWDCGCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPAYTYNNITCASP 586
                                                                                              RNRLAELPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNNSLRTFTPQPP
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SYSTEM: PC-DOS/MS-DOS
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N: 514
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protein complex, Fig. 32
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Pred. No. 1.5e-24;
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                                                                                                                                                                                       ----HRAAFRGLSRLTILYLF 235
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                 Matches 109;
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APPLICANT: Mochly
APPLICANT: Ron, D
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
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INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
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LENGTH: 605 amino acids
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REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
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                                  236 NNSLASLPGEALADL-----
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Washington
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                                                                                                                                                                                                                               83 --NLLTLWLFSNNLSTIYPGTFRHLQALEELDLGDNRHLRSLEPDTFQGLERLQSLHLYR 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
                                                                                                      GLGSLDRLLLHGNRLQGV----
                                                                                                                                       NQLQEVKAGAFLGLTNVAVMNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRTRPHTFT
RNRLAELPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNNSLRTFTPQPP 526
                                                                 GLSGLRRLFLKDNGLVGIEEQSLWGLAELLELDLTSNQLTHLPHR-LFQGLGKLEYLLLS 466
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02) 887-0763
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Pred. No. 1.5e-24;
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CURRENT APPLICATION NUMBER: US/09/063,950C
CURRENT FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 9
SOFWARE: Patentin Ver. 2.0
FQ ID NO 5
ENGTH: 605
TYPE: PAT
ORGANISM: Papio hamadryas
US-09-063-950-5
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                                                                                                                Sequence 49, Application US/08190802A Patent No. 5519003 GENERAL INFORMATION:
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Matches
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PATENT NO. 6225085
GENERAL INFORMATION:
APPLICANT: HOLIZMAN, Douglas A.
TITLE OF INVENTION: HOYEL LASG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: MEI-019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
            APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                               536 NPWDCSCPLKALRDFALQNPSAVPREVQAICEGDDCQPPVYTYNNITCASPPEVAGLDLR 595
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les 122; Conserv
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RESULT 4
US-08-477-346-49
; Sequence 49, Application US/08477346
; Patent No. 6262023
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Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 324-09
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/01
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                          587
                                                                                                                                              292 PERQGRDLRALREADFQAC 310
                                                                                                                                                                                 527 GLERLWLEGNPWDCGCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPAYTYNNITCASP
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                                                                                                                                                                                                                                                                                       236 NNSLASLPGEALADL------
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                                                                                                                       PEVVGLDLRDLSEAHFAPC
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28.8%; Pred. No. 1.56
Live 33; Mismatches
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-49:
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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  number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Gapop 10.0 , Gapext 0.5
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  MLPGLRRLLQAPASACLLLM......
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US-09-063-950-2
US-08-190-802A-49
US-08-477-346-49
US-08-477-346-50
US-08-487-072A-50
US-08-487-072A-50
US-08-487-072A-50
US-08-487-072A-50
US-08-190-802A-7-7
US-09-191-647-7
US-09-182-024A-5
PCT-US91-09055-2
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QY 319 GSRARGNSSSNHLYGVAEAGAPPADPSTLYRDLPAEDSRGRQGGDA	ERQGRDLRALREADFQACPPAA :	QY 209 LLHGN-RLQGVHRAAFRGLSRLTILYLFNNSLASLPGEALADLPSLEFLRI 	QY 172 DDLFADLANLSHLFLHGNRLRLLTEHVFDDL 186 PGIL-DTANVEALRLAGLGLQCLDEGLFSRLRNLHDLDVSDNQLERVPPV	Qy 112 DIGDNRHLRSLEPDTFOGLERLQSLHLYRCQLSSLPGNIFRGLYSLQYLYI	QY 78 GTEGSNLLTLWLESNNLSTIYPGTERHL	DRLF : VGLY	Query Match 16.6%; Score 369; DB 4; Length 6 Best Local Similarity 30.8%; Pred. No. 2.2e-26; Matches 141; Conservative 36; Mismatches 181; Indels	RESULT 1 US-09-063-950-2 US-09-063-950-2 Sequence 2, Application US/09063950C Patent No. 6225085 GENERAL INFORMATION: APPLICANT: HOltzman, Douglas A. TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MO TITLE OF INVENTION: THEREFOR FILE REFERENCE: MEI-019 FILE REFERENCE: MEI-019 CURRENT APPLICATION UNUMBER: US/09/063,950C CURRENT FILING DATE: 1998-04-21 NUMBER OF SEQ ID NOS: 9 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 673 TYPE: PRT ORGANISM: Homo sapiens US-09-063-950-2	ALIGNMENTS	28 278.5 12.5 1091 3 US-08-986-485-5 529 278.5 12.5 1101 3 US-08-986-485-2 539 261.5 11.7 222 5 PCT-US91-09055-3 58 253 11.4 307 1 US-08-986-482-063A-48 52 53 11.4 342 1 US-08-272-919-2 58 253 11.4 342 1 US-08-313-4 58 253 11.4 353 6 5340334-4 353 11.4 353 6 5340334-4 58 253 11.4 359 1 US-08-303-238-4 58 34 4 231.5 10.4 1112 28 2 1 US-08-353-585-2 58 231.5 10.4 1112 4 US-09-353-585-2 58 34 4 217.5 9.8 373 4 US-09-353-585-3 58 58 34 4 217.5 9.8 373 4 US-09-724-864-43 58 58 38 38 38 38 38 38 38 38 38 38 38 38 38
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